

Access DB# 97681

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4445</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>6/30/03</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>6/30/03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>2</u>	Other _____	Other (specify) _____



[illegible]

Quincy Match Co., Inc., 601 Broadway, Boston, Mass. 02116; Best Lock Manufacturing Co., Inc., 201 N. 6th St., Milwaukee, Wis. 53204; M. J. & J. J. Manufacturing Co., 1000 N. 1st St., Milwaukee, Wis. 53204.

1. $\mathcal{A} \subseteq \mathcal{B}$ and $\mathcal{B} \subseteq \mathcal{A}$ are both true.
 2. $\mathcal{A} \subseteq \mathcal{B}$ and $\mathcal{B} \subseteq \mathcal{A}$ are both false.
 3. $\mathcal{A} \subseteq \mathcal{B}$ and $\mathcal{B} \subseteq \mathcal{A}$ are both true.
 4. $\mathcal{A} \subseteq \mathcal{B}$ and $\mathcal{B} \subseteq \mathcal{A}$ are both false.

of Domestically produced goods. The results for exports are consistent with the findings of McFarland (1994) and McLeod (2001) that the export market is not a source of growth for the manufacturing sector in Mexico.

[illegible]

Δ : Molal heat of polymerization
 Δ_f : Molal heat of fusion of RNA
 Δ_r : Bond energy; 1.40 e.u.

Accepted for publication 10 May 2006
Published online 1 June 2006

[illegible]

Abstracts of the 1999 Meeting of the American Society of Human Genetics, 15-19 Nov 1999, Houston, Texas, 1-100. *Am J Hum Genet* 65:1-100, 1999

Submitted to the EMIS 2014 conference
 Accepted for publication : 2014/06
 Accepted for publication : 2014/06

A Molecular Weight of 100,000
 A Pore Diameter of 1.44 μ m
 A Pore Volume of 0.65 cm³/g
 A Surface Area of 100 m²/g

1. *Staphylococcus aureus* (1000)
 2. *Staphylococcus aureus* (1000)
 3. *Staphylococcus aureus* (1000)
 4. *Staphylococcus aureus* (1000)
 5. *Staphylococcus aureus* (1000)
 6. *Staphylococcus aureus* (1000)
 7. *Staphylococcus aureus* (1000)
 8. *Staphylococcus aureus* (1000)
 9. *Staphylococcus aureus* (1000)
 10. *Staphylococcus aureus* (1000)

Journal of Management Inquiry 20(4) 409–424
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DOI: 10.1177/1056492611416111
<http://jmi.sagepub.com>

[illegible]

T

[illegible][illegible]

Abolitionists' Journal: A Journal of Literature, Science, and Art, Vol. 1, No. 1, 1840

Address: 1244 P.P.
Aptos 94920, Santa Cruz, CA 95061
Tel: 408/255-1001

Abstract—The authors examined the effects of a 12-week, 1000 kcal energy deficit diet on the body composition and metabolic profile of 10 obese women. The subjects were randomly assigned to either a low-carbohydrate or a low-fat diet. The low-carbohydrate diet was composed of 15% carbohydrate, 65% fat, and 20% protein, and the low-fat diet was composed of 55% carbohydrate, 30% fat, and 15% protein. Both diets were supplemented with 100 mg of vitamin E daily. The subjects were monitored for changes in body weight, body composition, and metabolic profile. The low-carbohydrate diet resulted in a greater loss of body weight and a greater loss of body fat than the low-fat diet. The low-carbohydrate diet also resulted in a greater increase in HDL cholesterol and a greater decrease in triglyceride levels than the low-fat diet. The authors conclude that a low-carbohydrate diet is more effective than a low-fat diet for promoting weight loss and improving metabolic profile in obese women.

Best Local Similarity: 0.9999; Prod. No.: 647
 Molecule: *l*-Tryptophan; Molecular Weight: 204.23
 Molar Mass: 204.23

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JAN 11 1966
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WASHINGTON, D.C.

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

[illegible][illegible][illegible]

Quincy March	1918	Score 1	1918	Score 1
Post local similarity	1918	1918	1918	1918
Marches	1918	1918	1918	1918

the *Phrynosoma* spp. and *Uta* spp. are the most common species found in the study area. The *Phrynosoma* spp. are found in the open areas, while the *Uta* spp. are found in the wooded areas. The *Phrynosoma* spp. are found in the open areas, while the *Uta* spp. are found in the wooded areas. The *Phrynosoma* spp. are found in the open areas, while the *Uta* spp. are found in the wooded areas.

1. *Staphylococcus aureus* (ATCC 12228)
 2. *Staphylococcus aureus* (ATCC 12228)
 3. *Staphylococcus aureus* (ATCC 12228)
 4. *Staphylococcus aureus* (ATCC 12228)
 5. *Staphylococcus aureus* (ATCC 12228)
 6. *Staphylococcus aureus* (ATCC 12228)
 7. *Staphylococcus aureus* (ATCC 12228)
 8. *Staphylococcus aureus* (ATCC 12228)
 9. *Staphylococcus aureus* (ATCC 12228)
 10. *Staphylococcus aureus* (ATCC 12228)

A. S. J. J. Koolen, *1991*
 A. M. J. J. Koolen, *1991*
 A. M. J. J. Koolen, *1991*
 A. M. J. J. Koolen, *1991*

[illegible]

[illegible][illegible]

```

Matches: 0, Uncovered: 0, Mismatches: 0, Indels: 0, Gap:
0  345 STANDARD 102
    |||||
Dr  179 STANDARD 185

RESULT 30
FLAG: FPRAB
ID: FLAB PYRAE STANDARD: FRT: 345 AA
AC: 345TTS;
TT 15-JUN-2002 (98) 41: 345TTS(1)
CT 15-JUN-2002 (98) 41: 1st sequence update
DT 15-JUN-2002 (98) 41: 1st annotation update
DE Acidic ribosomal protein P0 homolog (L10F)
GN RPLP0 OR PAB107.
OC Pykarchaeum acrophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
    |||

```

[illegible]

[illegible][illegible]

GenCore version 5.1.6
Copyright (c) 1994 - 2003 Computer 1.0

OM FRT-01 - Protein search, using sw method

Run on: Jun 30, 2003, 14:14:43, Search time: 19 Seconds
Without alignment: 2261235 Million cells updated/Sec

Title: US-09-905-744B-6

Perfect score: 428

Sequence: 1 MATSWTVEFWIVGQVQCA

Scoring table:

Gap: 60 0, Gap: 60 0

Search: 671560 seqs, 20647115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671560

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database

1: SP_archaea.*
2: SP_bacteria.*
3: SP_fungi.*
4: SP_human.*
5: SP_invertebrate.*
6: SP_mammal.*
7: SP_mbc.*
8: SP_organelle.*
9: SP_phage.*
10: SP_plant.*
11: SP_protist.*
12: SP_virus.*
13: SP_vertebrate.*
14: SP_unclassified.*
15: SP_virus.*
16: SP_bacteriophage.*
17: SP_archaeap.*

Prod No: 15 - the number of results produced by choice 1, here 3
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Database
1	400	91.6	407	4	06XEB3	GenBank: Homo sapiens
2	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
3	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
4	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
5	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
6	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
7	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
8	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
9	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
10	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
11	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
12	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
13	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
14	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
15	355	93.2	412	4	06XEB3	GenBank: Homo sapiens
16	355	93.2	412	4	06XEB3	GenBank: Homo sapiens

17	17	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
18	18	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
19	19	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
20	20	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
21	21	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
22	22	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
23	23	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
24	24	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
25	25	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
26	26	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
27	27	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
28	28	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
29	29	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
30	30	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
31	31	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
32	32	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
33	33	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
34	34	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
35	35	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
36	36	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
37	37	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
38	38	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
39	39	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
40	40	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
41	41	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
42	42	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
43	43	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
44	44	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
45	45	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
46	46	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
47	47	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
48	48	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
49	49	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
50	50	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
51	51	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
52	52	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
53	53	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
54	54	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
55	55	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
56	56	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
57	57	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
58	58	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
59	59	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
60	60	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
61	61	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
62	62	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
63	63	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
64	64	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
65	65	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
66	66	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
67	67	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
68	68	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
69	69	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
70	70	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
71	71	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
72	72	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
73	73	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
74	74	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
75	75	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
76	76	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
77	77	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
78	78	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
79	79	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
80	80	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
81	81	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
82	82	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
83	83	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
84	84	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
85	85	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
86	86	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
87	87	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
88	88	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
89	89	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
90	90	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
91	91	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
92	92	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
93	93	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
94	94	8	1	9	418	10	06XEB3	GenBank: Homo sapiens
95	95	8	1	9	418	10	06XEB3	GenBank: Homo sapiens


```

OC Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Strausberg R.
RT S. pyramical (Tremblor) 13, last sequence update.
DR EMBL: BC011241; AAL1241.1;
DR MBL: MGI:106663; EMBL:
DE Tissue: IP000407; GDAI_CD39_NTFase.
DP Pfam: PF01501; GDAI_CD39_1;
PF PROSITE: PS01232; GDAI_CD39_NTFase; UNIPROT:
KW Hydroxylase.
SQ
SEQUENCE 485 AA; 1419 MW; AATGAGGATGAGAGGCTGCTG.
Query March 2 68 Score 119.00 Length 485
Best Local Similarity 100.0%; Freq No. 20157.
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 159 DMSASTSTR 204
DB 201 DMSASTSTR 211
RESULT 10
Query:
AC Q9D813 PRELIMINARY; FRT; 308 AA.
ID Q9D813;
AC Q9D813;
DT 01-JUN-2001 (Tremblor) 17, Created.
DT 01-JUN-2001 (Tremblor) 17, last sequence update.
DE 01-JUN-2002 (Tremblor) 21, last annotation update.
DE 20102200901X.
CN 20102200901X.
CC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Strausberg R.
RT S. pyramical (Tremblor) 13, last sequence update.
DR EMBL: BC011241; AAL1241.1;
DR MBL: MGI:106663; EMBL:
DE Tissue: IP000407; GDAI_CD39_NTFase.
DP Pfam: PF01501; GDAI_CD39_1;
PF PROSITE: PS01232; GDAI_CD39_NTFase; UNIPROT:
KW Hydroxylase.
SQ
SEQUENCE 485 AA; 1419 MW; AATGAGGATGAGAGGCTGCTG.
Query March 2 68 Score 119.00 Length 485
Best Local Similarity 100.0%; Freq No. 20157.
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 159 DMSASTSTR 204
DB 201 DMSASTSTR 211

```

```

RESULT 11
Q9SPM6 PRELIMINARY; FRT; 455 AA.
ID Q9SPM6;
AC Q9SPM6;
DT 01-MAY-2000 (Tremblor) 13, Created.
DT 01-MAY-2000 (Tremblor) 13, last sequence update.
DE 01-MAY-2002 (Tremblor) 20, last annotation update.
DE 20102200901X.
CN 20102200901X.
CC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Strausberg R.
RT S. pyramical (Tremblor) 13, last sequence update.
DR EMBL: BC011241; AAL1241.1;
DR MBL: MGI:106663; EMBL:
DE Tissue: IP000407; GDAI_CD39_NTFase.
DP Pfam: PF01501; GDAI_CD39_1;
PF PROSITE: PS01232; GDAI_CD39_NTFase; UNIPROT:
KW Hydroxylase.
SQ
SEQUENCE 485 AA; 1419 MW; AATGAGGATGAGAGGCTGCTG.
Query March 2 68 Score 119.00 Length 485
Best Local Similarity 100.0%; Freq No. 20157.
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 159 DMSASTSTR 204
DB 201 DMSASTSTR 211

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Y. S. WANG, H. T. CHEN, S. C. CHEN

RECEIVED FOR N.A.


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RESULT 31
Q98039 098039 PRELIMINARY PRT 66 AA
AC Q98039
DT 01-NOV-1996 (TRENDS) 01, Created
DT 01-NOV-1996 (TRENDS) 01, Last sequence update
DT 01-DEC-2001 (TRENDS) 19, Last annotation update
DE Hypothetical 7.9 kDa protein
OS La France disease virus
OC Viruses, unclassified viruses
CX NPI_taxid:29773
FN
FP SEQUENCE FROM N A
FC STRAIN:NEW
EX MEMPRO-011964, PubMed:99122
AA Resid P.A., Wright P.J.,
RT "RT-PCR detection of ASPs associated with La France disease of the
RT cultivated mushroom Agaricus bisporus (Fr.) Sing. (Basidiomycota)".
RL J. Virol. Methods 63:17-26(1999)
DP EMBL: U6240; AB064778.1
KW Hypothetical protein
SC SEQUENCE 66 AA, 7920 MW, 119460001404.00064.

Query Match 16; Score 7; DR 12; Length 66;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7, Conservation 0, Mismatches 0, Indels 0, Gaps 0

QY 307 VAFVPR 313
DB 14 VLPVPR 20

RESULT 32
Q95L31 095L31 PRELIMINARY PRT 74 AA
AC Q95L31
DT 01-DEC-2001 (TRENDS) 19, Created
DT 01-DEC-2001 (TRENDS) 19, Last sequence update
DT 01-MAR-2001 (TRENDS) 29, Last annotation update
DE Amino acid transporter Slc7a6 (Fragment)
GN Slc7a6
OS Equisetum arvense (L.) L.
OC Equisetidae; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Perissodactyla; Equidae; Equus
CX NCBI_taxid:9796;
RN
PP SEQUENCE FROM N A
RA Harawa K., Leati T., Bailey E.,
RT "Mapping of a gene for resistance to a viral disease of horses and
RT amino acid transporters (SLC7A6 and SLC7A5) and analysis for effect
RT of polymorphism on genetic fragility of red blood cells".
P. Submitted (SFP-2001) to the EMBL/GenBank/CCDB database
DP EMBL: AF45523; AA109611.1
DE InterPro: IPR00220; AA101_Protein
FT MPTTP 1
FT NCTTP 74
FT NCTTP 74
SC SEQUENCE 74 AA, 7921 MW, 79475400714400.00064.

Query Match 16; Score 7; DR 12; Length 66;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7, Conservation 0, Mismatches 0, Indels 0, Gaps 0

QY 252 LATGAL 258
DB 19 LATGAL 25

RESULT 33
Q9HX96 09HX96 PRELIMINARY PRT 53 AA
AC Q9HX96
DT 01-MAR-2001 (TRENDS) 15, Created
DT 01-MAR-2001 (TRENDS) 15, Last sequence update

```

```

DT 01-MAR-2001 (TRENDS) 21, Last annotation update
DE Molybdopterin converting factor, small subunit.
CX NCBI_taxid:503917.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Gammaproteobacteria;
OC Pseudomonas.
CX NCBI_taxid:503917.
FN
FP SEQUENCE FROM N A
FC STRAIN:ATCC 15692 / PAOI;
EX MEDLINE:2843733; PubMed:1094493;
RA Slover C.K., Pham X.-O.T., Erwin A.L., Muzyczka S.D., Marmorek E.,
RA Hickey M.J., Blumhagen F.C., Hultquist W.C., Kaulsky R.L.,
RA Goffin R.L., Goffin T., Goffin F., Westhead W.D.,
RA Smith R.A., Goffin P.H., Wong G.K.S., Wu J.,
RA Felder J., Goffin W.H., Hultquist P.W., Goffin W.J.,
RT "Molybdopterin converting factor (MCF) from Pseudomonas aeruginosa PAOI an
RT alternative genetic pathway?".
P. Nature 406:959-964(2000)
DP EMBL: AB064803; AA07204.1
DE InterPro: IPR017490
DR InterPro: IPR01749; This.
DP Pfam: PF01597; pf0170; 1.
KW Complete proteome.
SC SEQUENCE 53 AA, 5920 MW, 1144550001400.00064.

Query Match 16; Score 7; DR 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7, Conservation 0, Mismatches 0, Indels 0, Gaps 0

QY 252 LATGAL 258
DB 27 LATGAL 33

RESULT 34
Q9WZC0 09WZC0 PRELIMINARY PRT 38 AA
AC Q9WZC0
DT 01-MAR-2002 (TRENDS) 20, Created
DT 01-MAR-2002 (TRENDS) 20, Last sequence update
DT 01-MAR-2002 (TRENDS) 20, Last annotation update
DE CAP59 protein (Fragment)
GN CAP59
OS Cryptosporidium parvum (Feline)
OC Eukaryota; Fungi; Fungi; Zygomycota; Zygomycetes; Zygomycetes; Zygomycetes;
OC Zygomycetes; Zygomycetes; Zygomycetes; Zygomycetes; Zygomycetes; Zygomycetes;
CX NCBI_taxid:100000000;
RN
PP SEQUENCE FROM N A
RA Saito T., Kishi T., Chikada T.,
RT "Cloning and characterization of CAP59, a protein of Cryptosporidium
RT parvum, a sequence analysis of multiple genes and a chaperone
RT activity of CAP59 protein".
P. Microbiol. Immunol. 45:767-768(2001).
DE EMBL: AB066115; BA07201.1
DE EMBL: AB066116; BA07202.1
DE EMBL: AB066117; BA07203.1
DE EMBL: AB066118; BA07204.1
DE EMBL: AB066119; BA07205.1
DE EMBL: AB066120; BA07206.1
DE EMBL: AB066121; BA07207.1
DE EMBL: AB066122; BA07208.1
DE EMBL: AB066123; BA07209.1
DE EMBL: AB066124; BA07210.1
DE EMBL: AB066125; BA07211.1
DE EMBL: AB066126; BA07212.1
DE EMBL: AB066127; BA07213.1
DE EMBL: AB066128; BA07214.1
DE EMBL: AB066129; BA07215.1

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DT 01-NOV-1998 (TRENBLER) 08, Last sequence update)
 DT 01-DEC-2001 (TRENBLER) 19, Last annotation update)
 DE Gp120 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1
 CC Viruses; Retroid viruses; Retroviridae; Lentiviruses
 CX NCBI_TaxID:11676;
 RN
 PP SEQUENCE FROM N.A.
 RC STRAIN=96CH17;
 RX MEDLINE 2914662, Pubmed:10024057;
 RA Chen J, Young N L, Subbarao S, Marichit P, Sanguanwongse S,
 PA McCosker S, Jayaram C, Luo C C, Mastror T D, Liang J,
 RT HIV type 1 subtypes in Guangxi Province, China, 1996.";
 RI AIDS Res Hum Retroviruses 15:81-84(1999).
 DR FMRU, AF090312, AF090402;
 DE Interpro: IPR000777; Gp120
 DR Pfam, PF00516, PF170,
 KW AIDS, Coat Protein, Glycoprotein
 FT NON-TER 1
 FT NON-TER 1
 ST SEQUENCE 115 AA, 17710 MW, 3192544 Da, 17710 MW, 3192544 Da, 17710 MW, 3192544 Da

Query Match 1.68; Score 7; DB 15; Length 115;
 Best Local Similarity 100.0%; Pos: 1; 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 EXTEND 220
 DB 63 EXTEND 69

RESULT 19
 09:520
 ID 09F820 FREEDMINARY, ENT, 123 AA.
 AC 09F820;
 DT 01-MAR-2001 (TRENBLER) 16, Created)
 DT 01-MAR-2001 (TRENBLER) 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLER) 01, Last annotation update)
 DE Ayras (Fragment)
 OS Pisum sativum (Garden pea)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Eudicotyledones; Core eudicotyledones; Rosales;
 CC Eulsioidae; Fabales; Fabaceae; Papilionales; Viciae; Pisum
 CX NCBI_TaxID:3888;
 RN
 PP SEQUENCE FROM N.A.
 RC STRAIN=ALASKA; TISSE-DARY GROWN STEM INTERNOE;
 RA Yoneda M, Shibata K, Abe S;
 ST Submitted (JUL-1999) to the EMBL/GenBank/CCRC databases
 RN
 PP SEQUENCE FROM N.A.
 RC STRAIN=ALASKA; TISSE-DARY GROWN STEM INTERNOE;
 RA Shibata K, Abe S, Davies E;
 ST "Structure of the coding region and mRNA variants of the Yoneda M
 PT Pisum sativum";
 RI Agric Physiol Plant 20:313(2001);
 DR FMRU, AB010444; BAB189111;
 DR Interpro: IPR000407; Gp120; JIP120;
 DR Pfam: PF01150; Gp120; Gp120;
 FT NON-TER 123
 FT NON-TER 123
 ST SEQUENCE 123 AA, 17710 MW, 30441601 Da, 17710 MW, 30441601 Da, 17710 MW, 30441601 Da

Query Match 1.68; Score 7; DB 15; Length 115;
 Best Local Similarity 100.0%; Pos: 1; 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 FDAGSTG 59
 DB 48 FDAGSTG 54

RESULT 40

Q91844
 ID Q91844 FREEDMINARY, ENT, 133 AA.
 AC Q91844;
 DT 01-OCT-2000 (TRENBLER) 15, Created;
 DT 01-OCT-2000 (TRENBLER) 15, Last sequence update)
 DE 01-DEC-2001 (TRENBLER) 19, Last annotation update)
 GN ENV.
 OS Human immunodeficiency virus type 1
 CC Viruses; Retroid viruses; Retroviridae; Lentiviruses
 CX NCBI_TaxID:11676;
 RN
 PP SEQUENCE FROM N.A.
 RC STRAIN=96CH17;
 RX MEDLINE 2914662, Pubmed:10024057;
 RA Chen J, Young N L, Subbarao S, Marichit P, Sanguanwongse S,
 PA McCosker S, Jayaram C, Luo C C, Mastror T D, Liang J,
 RT HIV type 1 subtypes in Guangxi Province, China, 1996.";
 RI AIDS Res Hum Retroviruses 15:81-84(1999).
 DR FMRU, AF090312, AF090402;
 DE Interpro: IPR000777; Gp120
 DR Pfam, PF00516, PF170,
 KW AIDS, Coat Protein, Glycoprotein
 FT NON-TER 1
 FT NON-TER 1
 ST SEQUENCE 123 AA, 17710 MW, 3192544 Da, 17710 MW, 3192544 Da, 17710 MW, 3192544 Da

Query Match 1.68; Score 7; DB 15; Length 133;
 Best Local Similarity 100.0%; Pos: 1; 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 EXTEND 220
 DB 111 EXTEND 117

RESULT 41
 09:540
 ID 09F820 FREEDMINARY, ENT, 123 AA.
 AC 09F820;
 DT 01-MAR-2001 (TRENBLER) 16, Created)
 DT 01-MAR-2001 (TRENBLER) 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLER) 01, Last annotation update)
 DE Ayras (Fragment)
 OS Pisum sativum (Garden pea)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Eudicotyledones; Core eudicotyledones; Rosales;
 CC Eulsioidae; Fabales; Fabaceae; Papilionales; Viciae; Pisum
 CX NCBI_TaxID:3888;
 RN
 PP SEQUENCE FROM N.A.
 RC STRAIN=ALASKA; TISSE-DARY GROWN STEM INTERNOE;
 RA Yoneda M, Shibata K, Abe S;
 ST Submitted (JUL-1999) to the EMBL/GenBank/CCRC databases
 RN
 PP SEQUENCE FROM N.A.
 RC STRAIN=ALASKA; TISSE-DARY GROWN STEM INTERNOE;
 RA Shibata K, Abe S, Davies E;
 ST "Structure of the coding region and mRNA variants of the Yoneda M
 PT Pisum sativum";
 RI Agric Physiol Plant 20:313(2001);
 DR FMRU, AB010444; BAB189111;
 DR Interpro: IPR000407; Gp120; JIP120;
 DR Pfam: PF01150; Gp120; Gp120;
 FT NON-TER 123
 FT NON-TER 123
 ST SEQUENCE 123 AA, 17710 MW, 30441601 Da, 17710 MW, 30441601 Da, 17710 MW, 30441601 Da

Query Match 1.68; Score 7; DB 15; Length 154;
 Best Local Similarity 100.0%; Pos: 1; 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LBSLGT 426

PA Adams M. D., Celisner S. E., Holt F. A., Evans C. A., ...
 PA Amanatides P. G., Schmitt S. E., Li P. W., Hinkins E. A., ...
 PA Gouge P. A., Lewis S. E., Pichler S., Ashburner M., ...
 PA Sutton G. G., Workman U. P., Vardelli M. D., Zhang Q., ...
 PA Branton F. C., Fung Y. H. C., Plazek F. G., ...
 PA Wan K. H., Doyle G., Baker E. C., Holt S., ...
 PA Abell C. F., Ashburner M., Ashburner M., ...
 PA Ballew P. M., Bae J. A., Faxon-Davies J., ...
 PA Beese R. V., Reppas F. V., Eichen J. F., ...
 PA Borkova D., Portman M. F., Bouck J., ...
 PA Purkis K. C., Busan E. A., Miller H., ...
 PA Cherry J. M., Cawley S., Dahke C., ...
 PA de Pablo B., Delcher A., Deng Z., ...
 PA Dodson K., Dupp L. E., Finkes M., ...
 PA Durbin K. J., Evangelista C. C., ...
 PA Foster C. C., Gabelman A. E., ...
 PA Glodex A., Grogg P., Grotz H., ...
 PA Harris N. L., Harvey D., Helman T., ...
 PA Hartin P., Heston R. A., ...
 PA Jatali M., Kalner F., ...
 PA Jermol B. E., ...
 PA Lasko P., ...
 PA Liu X., ...
 PA McKelvey T., ...
 PA McEnt S. M., ...
 PA Nelson D. F., ...
 PA Palazzoli M., ...
 PA Palmeri V., ...
 PA Shue B. C., ...
 PA Spier E., ...
 PA Svirskas P., ...
 PA Wang T. Y., ...
 PA Williams S. M., ...
 PA Ye J., ...
 PA Zheng X. H., ...
 RA Gibbs A., ...
 RA "The genome sequence of *Thiosphaera melanospora*."
 RL Science 287 2182 (1999).
 RF EMPD, AF000470, ...
 RF FLYPase, F8303013, ...
 SC SEQUENCE 168 AA; 1490 MW; 9470D9E9C7AF17 ...

Query March 1.64; Score 7; DB 5; Length 193;
 Best Local Similarity 100.0%; Freq. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 3; Gaps 0.

CY 369 PFSGSP 410
 DB 35 STDQDI 41

RESULT 46
 005333 PRELIMINARY; PRT; 185 AA.

ID 005333
 AC 005333
 DT 01-JUN-1997 (TEMPREL 04, Created)
 DT 01-JUL-1997 (TEMPREL 04, Last sequence update)
 DT 01-MAR-2003 (TEMPREL 04, Last annotation update)
 DE Pori ATP synthase, subunit P
 OS ATP
 OS Prokaryote: *Thiosphaera melanospora* (strain ...)
 OC Bacteria, Proteobacteria, alpha subphylum ...
 OC Photobacter
 OX NCBI_Taxid 1661
 PY 11
 PE SEQUENCE FROM N.A.
 RX MEDLINE=99035763; PubMed=9819357;
 RA Borgese R., Furuta P., Lambertini L., Melanetti R. A.,
 RT "The active site of the P subunit of the ATP synthase from
 RT the purple nonsulfur phototrophic bacterium *Thiosphaera*
 RT *capitata*." J. Arch. Microbiol. 170 390-394 (1999).
 DT Arch. Microbiol. 170 390-394 (1999).
 DB EMBL, Y13013, CAA0904

TE INFORMATION: PROTEIN: ATPase P11_...
 DB EMBL: F8303013; AF000470; ...
 SC SEQUENCE 168 AA; 1490 MW; 9470D9E9C7AF17 ...
 CY 369 PFSGSP 410
 DB 35 STDQDI 41

RESULT 47
 005333 PRELIMINARY; PRT; 193 AA.

ID 005333
 AC 005333
 DT 01-MAY-2000 (TEMPREL 11, Created)
 DT 01-MAY-2000 (TEMPREL 11, Last sequence update)
 DT 01-MAR-2003 (TEMPREL 11, Last annotation update)
 DE PFSGSP protein.
 OS PFSGSP
 OS *Thiosphaera melanospora* (strain ...)
 OC Bacteria, Proteobacteria, alpha subphylum ...
 OC Photobacter
 OX NCBI_Taxid=40410
 PY 11
 PE SEQUENCE FROM N.A.
 RX MEDLINE=99035763; PubMed=9819357;
 RA Borgese R., Furuta P., Lambertini L., Melanetti R. A.,
 RT "The active site of the P subunit of the ATP synthase from
 RT the purple nonsulfur phototrophic bacterium *Thiosphaera*
 RT *capitata*." J. Arch. Microbiol. 170 390-394 (1999).
 DT Arch. Microbiol. 170 390-394 (1999).
 DB EMBL, Y13013, CAA0904

13. 140 LAT: 50.100

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84 1 1 43 1 AATG134
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XX Drosophila melanogaster. 11-01-03. cell signalling. 11-01-03.
 KW pharmaceutical.
 XX
 XX Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 27-MAP-2001; 2001WO-0500291.
 XX
 XX 23-MAP-2000; 2000US-19-617P.
 XX
 XX 11-JUL-2000; 2000US-07-41P.
 XX
 XX (PENE) PE CORE NT.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI, 2001 656660/75.
 XX
 XX N-PSDB; AB010316.
 XX
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 XX Disclosure: SEQ ID NO 6431, 21P - Sequence listing: English.
 XX
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genetic DNA sequences (AB010316-AB010317), expressed DNA
 CC sequences (AB010490-AB010491) and the encoded proteins
 CC (AB010737-AB010739).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wpi.int/pub/published_pat_sequences.
 XX
 XX Sequence 461 AA;
 XX
 XX Query March 2003; Score 12; DB 22; Length 461;
 XX Fast Local similarity 100%; Prod N 2003;
 XX Marches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 126 VKRATAGRLRP 137
 XX |||||
 XX 156 VKRATAGRLRP 167
 XX
 XX RESULT 36
 XX ID ABB59611 standard; Protein: 464 AA
 XX
 XX ABB59611;
 XX
 XX 27-MAP-2000 (first entry)
 XX
 XX Drosophila melanogaster polypeptide SEQ ID NO 5625.
 XX
 XX Drosophila melanogaster polypeptide SEQ ID NO 5625.
 KW pharmaceutical.
 KW pharmaceutical.
 XX
 XX Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 23-MAP-2000; 2001WO-0500291.
 XX
 XX 11-JUL-2000; 2000US-07-41P.
 XX

PR 11-JUL-2000; 2000US-061415C.
 XX
 XX (PENE) PE CORE NT.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI, 2001-656660/75.
 XX
 XX N-PSDB; AB010314.
 XX
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 XX Disclosure: SEQ ID NO 6031, 21P - Sequence listing: English.
 XX
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genetic DNA sequences (AB010316-AB010317), expressed DNA
 CC sequences (AB010490-AB010491) and the encoded proteins
 CC (AB010737-AB010739).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wpi.int/pub/published_pat_sequences.
 XX
 XX Sequence 464 AA;
 XX
 XX Query March 2003; Score 12; DB 22; Length 464;
 XX Fast Local similarity 100%; Prod N 2003;
 XX Marches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 126 VKRATAGRLRP 137
 XX |||||
 XX 156 VKRATAGRLRP 167
 XX
 XX RESULT 37
 XX ID ABB19882 standard; Protein: 464 AA
 XX
 XX ABB19882;
 XX
 XX 27-MAP-2000 (first entry)
 XX
 XX Human CD39L3 protein.
 XX
 XX Human; CD-39-like protein; CD39L3 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW cerebrovascular disease; wound healing; stroke; kidney; Alzheimer's disease; HIV/AIDS;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischaemia reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; vitreous detachment; anti-injury; neuroprotection;
 KW keratinocytes; keratinocyte growth; keratinocyte survival; keratinocyte
 KW antiinflammatory; nephropathy; gastroenteritis; vasculopathy.
 XX
 XX Homo sapiens.
 OS
 XX US635C447-B1.
 XX
 XX 46-FEB-2002.
 XX
 XX 27-MAP-2000; 2001WO-0500291.
 XX
 XX 23-MAP-2000; 2000US-061415C.
 XX
 XX (HUSO) HUSO INC.
 XX
 XX Chakrabarti, P.
 XX

XX 13-OCT-1999; 99WS-014541.
 XX 16-OCT-1999; 99WS-014585.
 XX 06-NOV-1999; 99WS-014746.
 XX 13-AUG-1999; 99WS-014910.
 XX (IMMUNEX CORP.
 PA (CORP.) CORPHEM RES FORM INC.
 XX Maliszewski CR, Gayle RB, Marcus AC)
 XX WPI: 2000-339219/29.
 XX N.PSRN: AAD00204
 XX
 XX Inhibiting platelet activation and recruitment, useful for treating a
 XX mammal suffering from unstable angina, myocardial infarction, stroke,
 XX coronary artery disease, and/or peripheral vascular disease, including
 XX polypeptides.
 XX
 XX Example 9: Page 109-111; 118pp; English.
 XX
 XX The present sequence is encoded by soluble CD39 (CD39) expression
 XX plasmid. This was used for the transient expression of soluble protein in
 XX mammalian expression systems. Soluble CD39 is used in the treatment of
 XX unstable angina, myocardial infarction, stroke, coronary artery disease,
 XX or injury of the arteries, peripheral vascular disorders including lung
 XX embolism, platelet-associated ischemic disorders including lung
 XX embolism, stroke, and cerebral ischemia, myocardial infarction,
 XX including coronary artery disease and peripheral ischemia, thrombotic
 XX intracranial thrombosis, peripheral artery thrombosis, venous thrombosis,
 XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 XX embolism (PE), transient ischemic attack. Soluble CD39 is also useful
 XX for prevention of thrombus formation in patients with cardiovascular disease,
 XX stenosis or reformation of blood vessels or stroke.
 XX
 XX Sequence 487 AA,
 XX
 XX Query Match: 21% Score 0, E: 21, Length 487,
 XX Best Local Similarity: 100.0%, Field No. 3.5,
 XX Matches: 0, Conservative: 0, Mismatch: 0, Indels: 0, Gaps: 0
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 XX 108 IDLOGASTQ 206
 XX 223 IDLOGASTQ 231
 XX
 XX RESULT 58
 XX AAY70921
 XX ID AAY70921 standard; Protein; 487 AA
 XX AAY70921,
 XX
 XX 17-AUG-2000 (first entry)
 XX
 XX Human soluble CD39 fusion protein construct, FIMDFAGSGLDQDQ,
 XX Soluble CD39 (CD39) human: Myristic activity, platelet activation,
 XX unstable angina, myocardial infarction, stroke, coronary artery disease,
 XX atherosclerosis, peripheral vascular disorders, thrombotic disorders, including
 XX platelet-associated ischemic disorders, thrombotic disorders including lung
 XX embolism, stroke, and cerebral ischemia, myocardial infarction,
 XX including coronary artery disease and peripheral ischemia, thrombotic
 XX intracranial thrombosis, peripheral artery thrombosis, venous thrombosis,
 XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 XX transient ischemic attack. Soluble CD39 is also useful for prevention of
 XX thrombus formation or reformation, occlusion, reocclusion, stenosis,
 XX stenosis or reformation of blood vessels or stroke.
 XX
 XX CS Homo sapiens
 XX CS Synthetic.
 XX
 XX Key location/Qualifiers
 XX FH 1:24
 XX FT Peptide
 XX FT /note: "Derived from human Interleukin 2 (IL2)"
 XX FT

XX Peptide 25-36
 XX /note: "Mouse human interleukin 2 (IL2) protein, 25-36"
 XX Region 37-40
 XX /note: "linker sequence"
 XX Region 41-48
 XX /note: "FLAG Tag sequence"
 XX Protein 49-487
 XX /note: "Human soluble CD39 protein"
 XX
 XX W020022459-A1.
 XX
 XX 27-APR-2000.
 XX
 XX 13-OCT-1999; 99WS-022955.
 XX
 XX 16-OCT-1999; 99WS-014585.
 XX 06-NOV-1999; 99WS-014746.
 XX 13-AUG-1999; 99WS-014910.
 XX
 XX (IMMUNEX CORP.
 XX
 XX Maliszewski CR, Gayle RB, Prior VL, Jarpe AC)
 XX WPI: 2000-339219/29.
 XX N.PSRN: AAD00204.
 XX
 XX The present sequence is the fusion protein construct FIMDFAGSGLDQDQ,
 XX comprising the soluble CD39 (CD39) protein region that has myristic activity, and
 XX a soluble CD39 (CD39) protein region that has myristic activity, and
 XX produces high levels of soluble protein in a mammalian expression system.
 XX transcribed cells. Soluble CD39 is constructed by joining the N- and
 XX C-terminal transmembrane domains. It encodes the soluble CD39 protein
 XX and the C-terminal transmembrane domain and the N-terminal myristic
 XX repeats ADP-activated platelet activation and recruitment, including
 XX platelet aggregation, soluble CD39 polypeptides and useful for treating
 XX angiosclerosis. It is useful for the treatment of unstable angina,
 XX myocardial infarction, stroke, coronary artery disease, coronary
 XX atherosclerosis, peripheral vascular disorders, thrombotic disorders,
 XX cerebral ischemia, thrombotic disorders including coronary artery disease,
 XX and cerebral artery thrombosis, intracranial and venous thrombosis,
 XX coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 XX transient ischemic attack. Soluble CD39 is also useful for prevention of
 XX thrombus formation or reformation, occlusion, reocclusion, stenosis,
 XX stenosis or reformation of blood vessels or stroke.
 XX
 XX Sequence 487 AA:
 XX
 XX Query Match: 21% Score 0, E: 21, Length 487,
 XX Best Local Similarity: 100.0%, Field No. 3.5,
 XX Matches: 0, Conservative: 0, Mismatch: 0, Indels: 0, Gaps: 0
 XX
 XX 108 IDLOGASTQ 206
 XX 223 IDLOGASTQ 231
 XX
 XX RESULT 59
 XX AAY33296
 XX ID AAY33296 standard; Protein; 487 AA.
 XX AAY33296,
 XX
 XX 06-NOV-1999 (first entry)
 XX
 XX Human membrane spanning protein MSP-1.
 XX DE



APPLICANT: Pan,James
 APPLICANT: Smith,Victoria
 APPLICANT: Matanabe,Colin K.
 APPLICANT: Wood,William I.
 APPLICANT: Chazy,Denis
 TITLE OF INVENTION: SEQUENCED AND TRANSPARENT POLYMERIDES AND NUCLEIC
 FILE REFERENCE: P44301042
 CURRENT FILING DATE: 2002-06-19
 CURRENT APPLICATION NUMBER: 09/077,450
 PRIOR APPLICATION REMOVED - See File Wrapper of Patm
 NUMBER OF SEQ ID NOS: 412
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-758-496

Query Match 21% Score 9, PP 3, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2.9,
 Matches 9/ Conservative 0/ Mismatches 0/ Indels 0/ Gaps 0/

QV 201 GGASTQITF 209
 DB 207 GGASTQITF 215

RESULT 21
 US-10-176-758-496

Sequence 496, Application US/10175758
 Publication No. US2003000343A1

GENERAL INFORMATION:
 APPLICANT: Baker,Kevin P.
 APPLICANT: Chen,Dian
 APPLICANT: Deshayes,Dan
 APPLICANT: Godowski,Paul J.
 APPLICANT: Gurevsky,Alexis L.
 APPLICANT: Par,James
 APPLICANT: Smith,Victoria
 APPLICANT: Matanabe,Colin K.
 APPLICANT: Wood,William I.
 APPLICANT: Chazy,Denis
 TITLE OF INVENTION: SEQUENCED AND TRANSPARENT POLYMERIDES AND NUCLEIC
 FILE REFERENCE: P44301042
 CURRENT APPLICATION NUMBER: US/10175758
 CURRENT FILING DATE: 2002-06-19
 PRIOR APPLICATION REMOVED - See File Wrapper of Patm
 NUMBER OF SEQ ID NOS: 412
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-758-496

Query Match 21% Score 9, PP 3, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2.9,
 Matches 9/ Conservative 0/ Mismatches 0/ Indels 0/ Gaps 0/

QV 201 GGASTQITF 209
 DB 207 GGASTQITF 215

RESULT 22

US-10-175-737-496

Sequence 496, Application US/10175737
 Publication No. US2003001153A1
 GENERAL INFORMATION:
 APPLICANT: Baker,Kevin P.
 APPLICANT: Chen,Dian
 APPLICANT: Deshayes,Dan

APPLICANT: Goddard,Audrey
 APPLICANT: Godowski,Paul J.
 APPLICANT: Gurevsky,Austin L.
 APPLICANT: Pan,James
 APPLICANT: Smith,Victoria
 APPLICANT: Matanabe,Colin K.
 APPLICANT: Wood,William I.
 APPLICANT: Chazy,Denis
 TITLE OF INVENTION: SEQUENCED AND TRANSPARENT POLYMERIDES AND NUCLEIC
 FILE REFERENCE: P44301050
 CURRENT APPLICATION NUMBER: US/10175737
 CURRENT FILING DATE: 2002-06-19
 PRIOR APPLICATION REMOVED - See File Wrapper of Patm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-175-737-496

Query Match 21% Score 9, PP 3, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2.9,
 Matches 9/ Conservative 0/ Mismatches 0/ Indels 0/ Gaps 0/

QV 201 GGASTQITF 209
 DB 207 GGASTQITF 215

RESULT 23

US-10-175-737-496

Sequence 496, Application US/10173737
 Publication No. US2003002293A1

GENERAL INFORMATION:
 APPLICANT: Baker,Kevin P.
 APPLICANT: Chen,Dian
 APPLICANT: Deshayes,Dan
 APPLICANT: Godowski,Paul J.
 APPLICANT: Gurevsky,Alexis L.
 APPLICANT: Par,James
 APPLICANT: Smith,Victoria
 APPLICANT: Matanabe,Colin K.
 APPLICANT: Wood,William I.
 APPLICANT: Chazy,Denis
 TITLE OF INVENTION: SEQUENCED AND TRANSPARENT POLYMERIDES AND NUCLEIC
 FILE REFERENCE: P44301050
 CURRENT APPLICATION NUMBER: US/10173737
 CURRENT FILING DATE: 2002-06-17
 PRIOR APPLICATION REMOVED - See File Wrapper of Patm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-175-737-496

Query Match 21% Score 9, PP 3, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2.9,
 Matches 9/ Conservative 0/ Mismatches 0/ Indels 0/ Gaps 0/

QV 201 GGASTQITF 209
 DB 207 GGASTQITF 215

RESULT 24

US-10-175-738-496

Sequence 496, Application US/10175738
 Publication No. US2003002294A1
 GENERAL INFORMATION:

RESULT 29

US-10-176-913-496

Sequence 496, Application US/10176913

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/176/913

CURRENT FILING DATE: 2002-06-25

Prior Application removed - See file wrapper of Paim

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 459

TYPE: PPT

ORGANISM: Homo Sapien

US-10-176-913-496

Query Match 2.1% Score 9, DB 9, Length 459,
 Best Local Similarity 100.0%, Pred. No. 2, 0,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

CV 207 GASTROTIF 215

DB 207 GASTROTIF 215

RESULT 29

US-10-180-552-496

Sequence 496, Application US/10180552

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/180/552

CURRENT FILING DATE: 2002-06-25

Prior Application removed - See file wrapper of Paim

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 459

TYPE: PPT

ORGANISM: Homo Sapien

US-10-180-552-496

Query Match 2.1% Score 9, DB 9, Length 459,
 Best Local Similarity 100.0%, Pred. No. 2, 0,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

CV 201 GASTROTIF 209

DB 207 GASTROTIF 215

RESULT 30

US-10-180-557-496

Sequence 496, Application US/10180557

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/180/557

CURRENT FILING DATE: 2002-06-25

Prior Application removed - See file wrapper of Paim

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PPT

ORGANISM: Homo Sapien

US-10-180-557-496

Query Match 2.1% Score 9, DB 9, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2, 0,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

CV 201 GASTROTIF 209

DB 207 GASTROTIF 215

RESULT 31

US-10-173-700-496

Sequence 496, Application US/10173700

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/173/700

CURRENT FILING DATE: 2002-06-17

Prior Application removed - See file wrapper of Paim

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PPT

ORGANISM: Homo Sapien

US-10-173-700-496

Query Match 2.1% Score 9, DB 9, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2, 0,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

CV 201 GASTROTIF 209

Matches 92 Conserved 92 Mismatched 0 Indels 0 Gaps 0

CY 201 GASTGITE 209

DB 207 GASTGITE 215

RESULT 42

US-10-174-592-496

Sequence 496, Application US/10174592

Publication No. US200302766A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Yan

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Guiney, Austin

APPLICANT: Watanabe, Victor

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEPTIC AND TRANSMEMBRANE PEPTIDES AND NOVEL

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

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FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

Query Match: 100% Score: 92, P4081324

Best Local Similarity: 100% of Conserved 92 Mismatched 0 Indels 0 Gaps 0

Matches 92 Conserved 92 Mismatched 0 Indels 0 Gaps 0

CY 201 GASTGITE 209

DB 207 GASTGITE 215

RESULT 34

US-10-174-592-496

Sequence 496, Application US/10174592

Publication No. US200302766A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Yan

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Guiney, Austin

APPLICANT: Watanabe, Victor

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEPTIC AND TRANSMEMBRANE PEPTIDES AND NOVEL

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

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FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

CURRENT FILING DATE: 2002/06/18

FILE REFERENCE: P4081324

TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-588-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100%, Prod. No. 2 9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 201 GGAAGCTT 209
DB 207 GGAAGCTT 215

RESULT 36
US-10-175-739-496

Sequence 496, Application US/10175739
Publication No. US2003027267A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Dian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Par, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091046

CURRENT APPLICATION NUMBER: 10/101779, 739

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Date

INVENTOR: 60/663742

SEQ ID NO 496

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-175-739-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100%, Prod. No. 2 9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 201 GGAAGCTT 209
DB 207 GGAAGCTT 215

RESULT 37
US-10-175-740-496

Sequence 496, Application US/10175740
Publication No. US2003027268A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Dian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Par, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091046

CURRENT APPLICATION NUMBER: 10/101779, 740

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Date

NUMBER OF SEQ ID NOS: 612
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-740-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100%, Prod. No. 2 9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 201 GGAAGCTT 209
DB 207 GGAAGCTT 215

RESULT 38
US-10-175-743-496

Sequence 496, Application US/10175743
Publication No. US2003027269A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Dian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Par, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091052

CURRENT APPLICATION NUMBER: 10/101779, 743

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Date

INVENTOR: 60/663743

SEQ ID NO 496

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-175-743-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100%, Prod. No. 2 9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 201 GGAAGCTT 209
DB 207 GGAAGCTT 215

RESULT 39
US-10-175-746-496

Sequence 496, Application US/10175746
Publication No. US2003027270A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Dian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Par, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091054

CURRENT APPLICATION NUMBER: 10/101779, 746

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Date

Query Match 2.1% Score 9; DB 3; Length 499;
 Best Local Similarity: 100.0%; Freq. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 39
 US-10-176-488-496

Sequence 496, Application US/10176488
 Publication No. US2003022721A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010119
 CURRENT APPLICATION NUMBER: US/10176488
 PRIOR APPLICATION REMOVED - See File Wrapper or Paim
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 499
 TYPE: PPT
 ORGANISM: Homo Sapiens
 US-10-176-488-496

Query Match 2.1% Score 9; DB 3; Length 499;
 Best Local Similarity: 100.0%; Freq. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 40
 US-10-176-492-496

Sequence 496, Application US/10176492
 Publication No. US2003022722A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010107
 CURRENT APPLICATION NUMBER: US/10176492
 PRIOR APPLICATION REMOVED - See File Wrapper or Paim
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 499
 TYPE: PPT

ORGANISM: Homo Sapiens
 US-10-176-492-496

Query Match 2.1% Score 9; DB 3; Length 499;
 Best Local Similarity: 100.0%; Freq. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 41
 US-10-176-747-496

Sequence 496, Application US/10176747
 Publication No. US2003022721A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010102
 CURRENT APPLICATION NUMBER: US/10176747
 PRIOR APPLICATION REMOVED - See File Wrapper or Paim
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 499
 TYPE: PPT
 ORGANISM: Homo Sapiens
 US-10-176-747-496

Query Match 2.1% Score 9; DB 3; Length 499;
 Best Local Similarity: 100.0%; Freq. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 42
 US-10-176-750-496

Sequence 496, Application US/10176750
 Publication No. US2003022721A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010103
 CURRENT APPLICATION NUMBER: US/10176750
 PRIOR APPLICATION REMOVED - See File Wrapper or Paim
 NUMBER OF SEQ ID NOS: 612

TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: 02/07/170,890
 CURRENT FILING DATE: 2002/06/21
 PRIOR APPLICATION REMOVED: See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-993-496

Query Match 2.1% Score 97 DB 9 Length 458
 Best Local Similarity: 100.00, Pctd No: 2.97
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 47
 US-10-176-993-496

Sequence 496, Application US/10176993
 Publication No. US20030032001A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND HOSTS
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: 02/07/170,890
 CURRENT FILING DATE: 2002/06/21
 PRIOR APPLICATION REMOVED: See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-993-496

Query Match 2.1% Score 97 DB 9 Length 458
 Best Local Similarity: 100.00, Pctd No: 2.97
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 48
 US-10-184-658-496

Sequence 496, Application US/10184658
 Publication No. US20030027281A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.

APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND HOSTS
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: US/10176,890
 CURRENT FILING DATE: 2002/06/21
 PRIOR APPLICATION REMOVED: See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-993-496

Query Match 2.1% Score 97 DB 9 Length 458
 Best Local Similarity: 100.00, Pctd No: 2.97
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 49
 US-10-173-695-496

Sequence 496, Application US/10173695
 Publication No. US20030032101A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND HOSTS
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: US/10173,695
 CURRENT FILING DATE: 2002/06/17
 PRIOR APPLICATION REMOVED: See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-173-695-496

Query Match 2.1% Score 97 DB 9 Length 458
 Best Local Similarity: 100.00, Pctd No: 2.97
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 50
 US-10-173-697-496

Sequence 496, Application US/10173697
 Publication No. US20030032102A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.


```

/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney/Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P430P109
/ CURRENT APPLICATION NUMBER: US/01/76,496
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION REMOVED - See file wrapper of P430P109
/ NUMBER OF SEQ ID NOS: 613
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-485-496

```

```

Query Match          2.1%, Score 9, DP 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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QY 201 GGAATGCTT 209
DB 207 GGAATGCTT 215

```

```

RESULT 58
US-10-176-487-496
/ Sequence 496, Application US/01/76487
/ Publication No. US2003032110A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney/Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P430P109
/ CURRENT APPLICATION NUMBER: US/01/76,496
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION REMOVED - See file wrapper of P430P109
/ NUMBER OF SEQ ID NOS: 613
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-487-496

```

```

QY 201 GGAATGCTT 209
DB 207 GGAATGCTT 215

```

```

Query Match          2.1%, Score 9, DP 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

```

QY 201 GGAATGCTT 209
DB 207 GGAATGCTT 215

```

```

RESULT 59
US-10-176-493-496
/ Sequence 496, Application US/01/76493
/ Publication No. US2003032111A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.

```

```

/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney/Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P430P109
/ CURRENT APPLICATION NUMBER: US/01/76,496
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION REMOVED - See file wrapper of P430P109
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-493-496

```

```

Query Match          2.1%, Score 9, DP 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

```

QY 201 GGAATGCTT 209
DB 207 GGAATGCTT 215

```

```

RESULT 60
US-10-176-756-496
/ Sequence 496, Application US/01/76756
/ Publication No. US2003032112A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney/Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P430P109
/ CURRENT APPLICATION NUMBER: US/01/76,756
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION REMOVED - See file wrapper of P430P109
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-756-496

```

```

Query Match          2.1%, Score 9, DP 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

```

QY 201 GGAATGCTT 209
DB 207 GGAATGCTT 215

```

```

RESULT 61
US-10-176-911-496
/ Sequence 496, Application US/01/76911

```


DL 207 GGASTOTTF 215

RESULT 65
US-10-179-510-496Sequence 496, Application US/10196510
Publication No. US200303117A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES

FILE REFERENCE: P34301018

CURRENT APPLICATION NUMBER: US/10196510

CURRENT FILING DATE: 2002-06-25

PRIORITY APPLICATION REMOVED - See File Wrapper of this

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-179-510-496

Query Match

Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches: 9, Conservative 0, Mismatches 0, Indels 0

Q7 201 GGASTOTTF 209

DB 207 GGASTOTTF 215

RESULT 66

US-10-180-543-496

Sequence 496, Application US/10190543
Publication No. US200303118A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES

FILE REFERENCE: P34301018

CURRENT APPLICATION NUMBER: US/10190543

CURRENT FILING DATE: 2002-06-25

PRIORITY APPLICATION REMOVED - See File Wrapper of this

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-180-543-496

Query Match

Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches: 9, Conservative 0, Mismatches 0, Indels 0

Q7 201 GGASTOTTF 209
DB 207 GGASTOTTF 215RESULT 67
US-10-180-544-496Sequence 496, Application US/10190544
Publication No. US200303118A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES

FILE REFERENCE: P34301018

CURRENT APPLICATION NUMBER: US/10190544

CURRENT FILING DATE: 2002-06-25

PRIORITY APPLICATION REMOVED - See File Wrapper of this

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-180-544-496

Query Match

Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches: 9, Conservative 0, Mismatches 0, Indels 0

Q7 201 GGASTOTTF 209

DB 207 GGASTOTTF 215

RESULT 68

US-10-180-546-496

Sequence 496, Application US/10190546
Publication No. US200303118A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES

FILE REFERENCE: P34301018

CURRENT APPLICATION NUMBER: US/10190546

CURRENT FILING DATE: 2002-06-25

PRIORITY APPLICATION REMOVED - See File Wrapper of this

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-180-546-496

SEQ ID NO 458
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-180-559-496

Query Match 21% Score 9, P: 9, Length 458;
Best Local Similarity: 100%, P: 1, N: 2, 3,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 201 GGASTQITF 209
DB 207 GGASTQITF 215

RESULT 73
US-10-181-000-496
Sequence 496, Application US/10181000
Publication No. US20030021056A1

GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
TITLE OF INVENTION: AIDS ENCODING THE SAME
FILE REFERENCE: P43090197
PRIORITY APPLICATION NUMBER: 09/094263
PRIORITY FILING DATE: 2002-06-26
PRIORITY APPLICATION REMOVED - See file wrapper or Paim
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-181-000-496

Query Match 21% Score 9, P: 9, Length 458;
Best Local Similarity: 100%, P: 1, N: 2, 3,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 201 GGASTQITF 209
DB 207 GGASTQITF 215

RESULT 74
US-10-183-010-496
Sequence 496, Application US/10183000
Publication No. US20030021056A1
GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
TITLE OF INVENTION: AIDS ENCODING THE SAME
FILE REFERENCE: P43090197
PRIORITY APPLICATION REMOVED - See file wrapper or Paim
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-183-010-496

CURRENT FILING DATE: 2002-06-26
PRIORITY APPLICATION REMOVED - See file wrapper or Paim
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-183-010-496

Query Match 21% Score 7, P: 7, Length 458;
Best Local Similarity: 100%, P: 1, N: 2, 3,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 201 GGASTQITF 209
DB 207 GGASTQITF 215

RESULT 75
US-10-183-012-496
Sequence 496, Application US/10183012
Publication No. US20030021077A1

GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
TITLE OF INVENTION: AIDS ENCODING THE SAME
FILE REFERENCE: P43090197
PRIORITY APPLICATION NUMBER: 09/094263
PRIORITY FILING DATE: 2002-06-26
PRIORITY APPLICATION REMOVED - See file wrapper or Paim
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-183-012-496

Query Match 21% Score 7, P: 7, Length 458;
Best Local Similarity: 100%, P: 1, N: 2, 3,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 201 GGASTQITF 209
DB 207 GGASTQITF 215

RESULT 76
US-10-183-012-496
Sequence 496, Application US/10183012
Publication No. US20030021077A1
GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
TITLE OF INVENTION: AIDS ENCODING THE SAME
FILE REFERENCE: P43090197
PRIORITY APPLICATION NUMBER: 09/094263
PRIORITY FILING DATE: 2002-06-26
PRIORITY APPLICATION REMOVED - See file wrapper or Paim
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-183-012-496

PRIP APPLICATION NUMBER: 60/080653

Query Match: 2.1%; Score 9; DB 3; Length 458;

Best Local Similarity: 100.0%; Prid No 2.3;

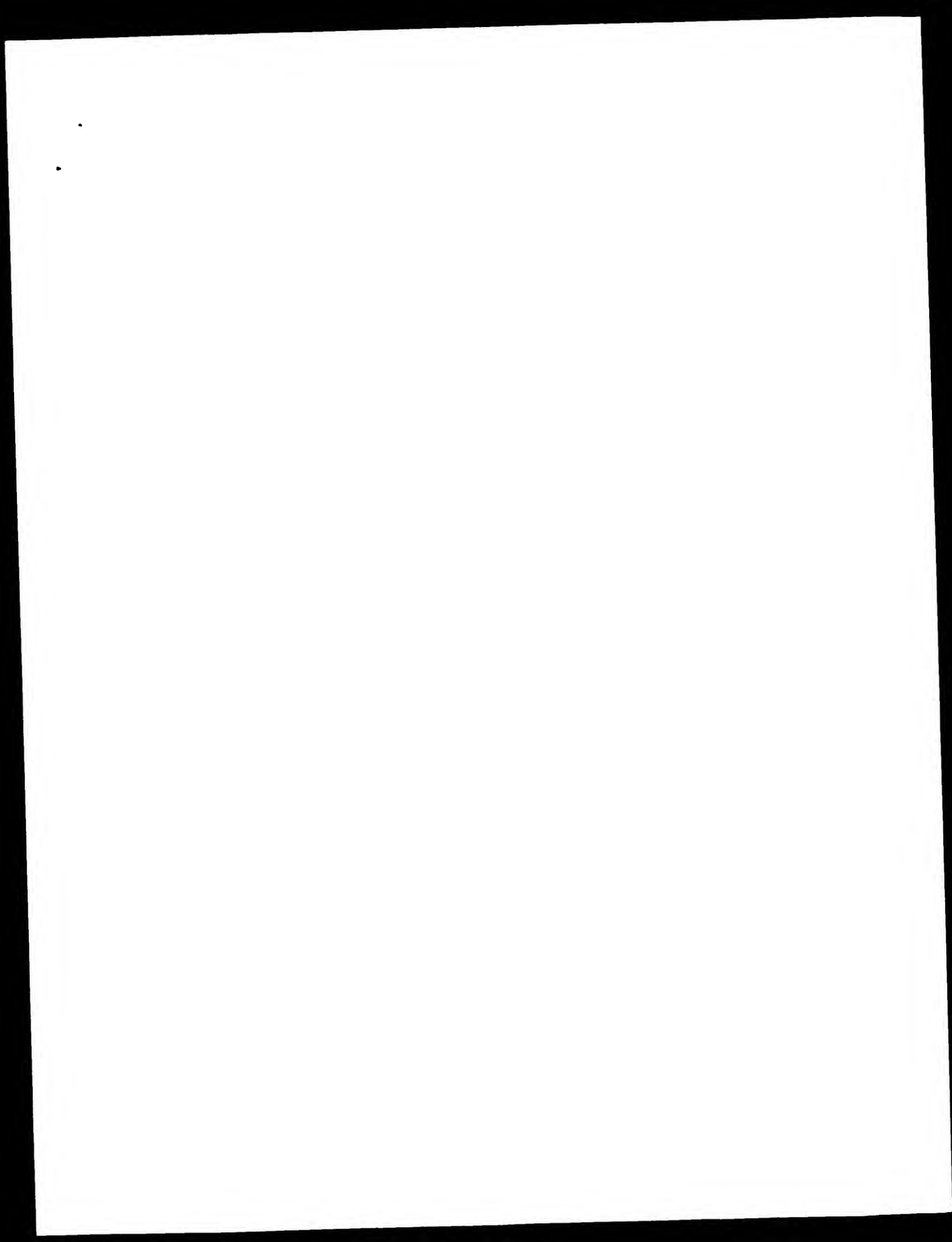
Matches: 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GASTOITF 209

DB 207 GASTOITF 215

Search completed: June 30, 2003, 15:07:13

tot time : 31 secs



EARLIER FILING DATE 1999-02-04
EARLIER APPLICATION NUMBER 09/122,449
EARLIER FILING DATE 1998-07-24
EARLIER APPLICATION NUMBER 09/122,449
EARLIER FILING DATE 1998-07-24
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-370-265-5

Query Match 100.0% Score 2250 DB 4 Length 428
Best Local Similarity 100.0% Freq No 200 246
Matches 428, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 MATMTVFEMVAVSVASVSHNLTWEELFUSWEPINVASIYINMEASISG 60
DE 1 MATMTVFEMVAVSVASVSHNLTWEELFUSWEPINVASIYINMEASISG 60
QY 61 FHVTFVQWVQVPLFLEDESEVSEVSEVSEVSEVSEVSEVSEVSEVSE 120
DE 61 FHVTFVQWVQVPLFLEDESEVSEVSEVSEVSEVSEVSEVSEVSEVSE 120
QY 121 KKTIVVAFATVPLFPLFHVAFALFVVEIFVSEVSEVSEVSEVSEVSE 180
DE 121 KKTIVVAFATVPLFPLFHVAFALFVVEIFVSEVSEVSEVSEVSEVSE 180
QY 181 NEVQV 240
DE 181 NEVQV 240
QY 241 SYLSEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 300
DE 241 SYLSEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 300
QY 301 EPCVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 360
DE 301 EPCVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 360
QY 361 EVQVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 420
DE 361 EVQVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 420
QY 421 LOSUGISH 428
DE 421 LOSUGISH 428

RESULT 9
US-09-608-285A-7
Sequence 7, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Muleto, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: POLYESTERS
FILE REFERENCE: 29110/31570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 09/583,331
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/567,400
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,228
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/447,167
PRIOR FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 09/422,449
PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-04-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-7

Query Match 99.8% Score 2235 DB 4 Length 428
Best Local Similarity 99.8% Freq No 1 48 246
Matches 425, Conservative 0, Mismatches 3, Indels 0, Gaps 0

QY 1 MATMTVFEMVAVSVASVSHNLTWEELFUSWEPINVASIYINMEASISG 60
DE 1 MATMTVFEMVAVSVASVSHNLTWEELFUSWEPINVASIYINMEASISG 60
QY 61 FHVTFVQWVQVPLFLEDESEVSEVSEVSEVSEVSEVSEVSEVSEVSE 120
DE 61 FHVTFVQWVQVPLFLEDESEVSEVSEVSEVSEVSEVSEVSEVSEVSE 120
QY 121 KKTIVVAFATVPLFPLFHVAFALFVVEIFVSEVSEVSEVSEVSEVSE 180
DE 121 KKTIVVAFATVPLFPLFHVAFALFVVEIFVSEVSEVSEVSEVSEVSE 180
QY 181 NEVQV 240
DE 181 NEVQV 240
QY 241 SYLSEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 300
DE 241 SYLSEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 300
QY 301 EPCVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 360
DE 301 EPCVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 360
QY 361 EVQVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 420
DE 361 EVQVAVLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 420
QY 421 LOSUGISH 428
DE 421 LOSUGISH 428

RESULT 10
US-09-350-836B-7
Sequence 7, Application US/09350836B
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Muleto, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: POLYESTERS
FILE REFERENCE: 29110/31570
CURRENT APPLICATION NUMBER: US/09/350,836B
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-04-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24

Case	Genotype	Phenotype	Age at onset	Age at death	Survival (years)	Notes
1	1	1	1	1	1	1
2	2	2	2	2	2	2
3	3	3	3	3	3	3
4	4	4	4	4	4	4
5	5	5	5	5	5	5
6	6	6	6	6	6	6
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[illegible]

GenCore version 5.1.6
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On protein - protein search, using sw model

Run on: Time 30, 2003, 14:34:27; Query time 21 seconds (without comments)

Title: IRS-99-905-744F-9050

Perfect score: 2250

Sequência: 1 MATSWGTVZFMILVNSNVNSA

FTGWAJGATPHI.081615H 428

Storing table: BLOSUM62

Gap: 10.0 , Gapext: 0.5

Searched: 110900 eqn, 4147000 ref:1109

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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[illegible]

Listing first 45 summaries

Summaries

Database : C:\WINNT\SYSTEM32\...

Pred. No. 15, the number of results reported by "none" + "low" + "some" greater than or equal to the score of the result being printed and is derived by analysis of the total score (see Table 1).

SUMMARIES

[illegible]

ATTACHMENTS

[illegible]

[illegible]

RESULT 3

FILE	MESSAGE
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	STANDARD;
	PRT;
	469 AA

[illegible][illegible]

...

[illegible][illegible]

RESULT 4

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[illegible]

PE 16-JUL-1999; SMD-US16180.
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 PE 16-JUL-1998; SMD-US18205.
 PE 24-JUL-1999; SMD-US18249.
 PE 04-FEB-1999; SMD-US24444.
 PE 19-MAR-1999; SMD-US27347.
 PE 09-JUL-1999; SMD-US28032.
 XX
 PA (HSE-) HSECO INC.
 XX
 PI Ford J, Mulero J;
 XX WPI: 2000-19397/10.
 D8 H-PSD9, A270107.
 XX
 PI New nucleic acid encoding human CD39-like protein, useful for treating
 PI and preventing thrombotic disease.
 XX
 ES Claim 17, Fig 6, 125pp; English.
 XX
 CC The present amino acid sequence is the CD39-L4 variant, designated
 CC as ACP III mutant protein, an apyrase and/or nucleoside diphosphatase
 CC (NDPase). It is isolated from the human foetal liver spleen cDNA library,
 CC HEPES320W. It is a soluble ATP diphosphatase, with a pI of 4.5 and a
 CC molecular weight of 38 kDa. It is involved in the hydrolysis of ATP, the substrate
 CC that causes platelet aggregation. CD39-L4 protein has 308 amino acids
 CC but only 1 human and mouse CD39. It has a pI of 4.5 and a molecular weight
 CC of 38 kDa. It is involved in the hydrolysis of ATP, the substrate for
 CC and anti-thrombotic activity. CD39-L4 is used to treat or prevent
 CC thrombotic, myocardial infarction, cerebral ischaemia and stroke. It is
 CC also used in vitro to maintain vessel in vitro during ex vivo perfusion
 CC circulation. It hydrolyses NDP as molecular weight markers and as
 CC nutritional supplements. It is used to identify thrombotic agents that
 CC bind and inhibit CD39-L4. It is designed to be used for the design of drugs
 CC to treat or prevent thrombotic disease.
 XX
 SQ Sequence 428 AA;
 Query Match 59.3% Score 2235 DP 21 Length 428;
 Best Local Similarity 99.3% Prod No 1 100000
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0

RESULT 6
 AAR72240
 ID AAR72240 (human); Protein: 308 AA.
 XX
 AC AAR72240;
 XX
 ID 14-MAY-2001 (first entry)
 XX
 DE Human CD39-like protein, CD39-L4 variant ACP III a nucleic acid sequence.
 XX
 XX Human CD39-like protein; apyrase; platelet function inhibitor;
 XX myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 XX cerebral artery blockage; platelet aggregation; inflammation;
 XX apoptosis; autoimmune disorder; neurological disorder; mutant; stroke;
 XX Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
 XX
 OS Homo sapiens.
 XX
 PN W0200110205-A1.
 XX
 PP 15-FEB-2001.
 XX
 EE CD39-L4 (human) (SMD-US16180).
 XX
 PP 06-AUG-1999; SMD-US17065.
 PP 11-AUG-1999; SMD-US17173.
 PP 26-SEP-2000; SMD-US17800.
 PP 26-MAY-2000; SMD-US18123.
 PP 21-JUN-2000; SMD-US18295.
 XX
 RA (HSE-) HSECO INC.
 XX
 FI Ford J, Mulero J, Young G;
 XX
 DI WPI: 2001-147489/15.
 DR N-PSD9; AAF63385.
 XX
 TT This sequence encodes human CD39-like protein, a nucleoside diphosphatase
 TT and apyrase activity. It is used to treat or prevent thrombotic
 TT disease, myocardial infarction, cerebral ischaemia and stroke.
 TT It is also used in vitro to maintain vessel in vitro during ex vivo
 TT perfusion and as a molecular weight marker and as a nutritional
 TT supplement.
 XX
 ES Claim 17, Fig 6, 125pp; English.
 XX
 CC This sequence encodes human CD39-like protein, a nucleoside diphosphatase
 CC and apyrase activity. It is used to treat or prevent thrombotic
 CC disease, myocardial infarction, cerebral ischaemia and stroke.
 CC It is also used in vitro to maintain vessel in vitro during ex vivo
 CC perfusion and as a molecular weight marker and as a nutritional
 CC supplement.
 XX
 CC This sequence encodes human CD39-like protein, a nucleoside diphosphatase
 CC and apyrase activity. It is used to treat or prevent thrombotic
 CC disease, myocardial infarction, cerebral ischaemia and stroke.
 CC It is also used in vitro to maintain vessel in vitro during ex vivo
 CC perfusion and as a molecular weight marker and as a nutritional
 CC supplement.
 XX
 CC This sequence encodes human CD39-like protein, a nucleoside diphosphatase
 CC and apyrase activity. It is used to treat or prevent thrombotic
 CC disease, myocardial infarction, cerebral ischaemia and stroke.
 CC It is also used in vitro to maintain vessel in vitro during ex vivo
 CC perfusion and as a molecular weight marker and as a nutritional
 CC supplement.
 XX
 SQ Sequence 428 AA;
 Query Match 59.3% Score 2235 DP 21 Length 428;
 Best Local Similarity 99.3% Prod No 1 100000
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0

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OK protein - protein search, using sw-meg-1

Prn on: June 30, 2003, 14:50:53, Search time 57.360000

(Without alignments)
902 478 Million Cells updated/sec

Title: US-09-905-744B 6

Perfect score: 250

Sequence: 1 MATSWTVFVPMVAVSCVCSAFTWAGVATHTLSTRTST 428

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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 42469

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:

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- 13: /cgn2-6/prodata/2/pubpa/ncsa_nhm_pfp.fpf*
- 14: /cgn2-6/prodata/2/pubpa/ncsa_nhm_pfp.fpf*

Prod No is the number of results generated by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

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43	250	100.0	428	US-10-176-750-496	Sequence 24, Afl1
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ALIGNMENTS

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1 MATSWTVFVPMVAVSCVCSAFTWAGVATHTLSTRTST 428
US-10-002-063-3

Query Match: 100.0, Length: 428
Post-local similarity: 100.0, E: 1.0e-200
Matrix: BLO62, Gap: 10, Gapext: 0.5, Indels: 0
1 MATSWTVFVPMVAVSCVCSAFTWAGVATHTLSTRTST 428
US-10-002-063-3

1 PRIOR APPLICATION NUMBER: US 08/044,234
 2 PRIOR FILING DATE: 10/02/98
 3 NUMBER OF SEQ ID NOS: 1
 4 SOFTWARE: Patent In 500 1.0
 5 SEQ ID NO: 1
 6 LENGTH: 462
 7 TYPE: PRN
 8 ORIGIN: Local Gen Bank
 9 US 09 173 51A 14

Query Match: 100% Score: 72 DB: 42 Length: 462
 Post Local Specificity: 100% Prod. No.: 10062
 Match: 72 Conservation: 0% Mismatches: 0% Indels: 0% Gaps: 0%

27 144 RFLP: 140
 28 173 51A 14

RESUME 41
 1 Sequence 14, Application 78/044,234
 2 Patent No. 6326472
 3 GENERAL INFORMATION:
 4 APPLICANT: Thomas, Jacqueline
 5 APPLICANT: Robert, J. deane's Edward Maria
 6 APPLICANT: Antonio
 7 APPLICANT: Sam, Theodore R.
 8 APPLICANT: Kazuo, R. Robert A.
 9 TITLE OF INVENTION: Human factor 1 protein, polypeptide and methods
 10 NUMBER OF SEQUENCES: 46
 11 PRESUMED ABSTRACT:
 12 ADDRESS: 1000 Research Blvd, Suite 100
 13 STREET: 900 California Avenue
 14 CITY: Palo Alto
 15 STATE: California
 16 COUNTRY: USA
 17 ZIP: 94304 1104
 18 COMPUTER REMARKS: PFM
 19 MODIFIER: PFM
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1 INFORMATION FOR SEQ ID NO: 14:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 462 amino acids
 4 TYPE: amino acid
 5 TOPOLOGY: linear
 6 MOLECULE TYPE: protein
 7 US 09 173 51A 14

Query Match: 100% Score: 72 DB: 42 Length: 462
 Post Local Specificity: 100% Prod. No.: 10062
 Match: 72 Conservation: 0% Mismatches: 0% Indels: 0% Gaps: 0%

27 144 RFLP: 140
 28 173 51A 14

RESUME 42
 1 Sequence 16, Application 78/044,234
 2 Patent No. 6326472
 3 GENERAL INFORMATION:
 4 APPLICANT: Thomas, Jacqueline
 5 APPLICANT: Robert, J. deane's Edward Maria
 6 APPLICANT: Antonio
 7 APPLICANT: Sam, Theodore R.
 8 APPLICANT: Kazuo, R. Robert A.
 9 TITLE OF INVENTION: Human factor 1 protein, polypeptide and methods
 10 NUMBER OF SEQUENCES: 46
 11 PRESUMED ABSTRACT:
 12 ADDRESS: 1000 Research Blvd, Suite 100
 13 STREET: 900 California Avenue
 14 CITY: Palo Alto
 15 STATE: California
 16 COUNTRY: USA
 17 ZIP: 94304 1104
 18 COMPUTER REMARKS: PFM
 19 MODIFIER: PFM
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LENGTH: 604 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-171-151A-16

Query Match 1.63 Score 71.22 41 Length 604
 Best Local Similarity 100.00, Prod No 126402
 Matches 7, Conservation 0, Mismatches 0, Indels 0, Gaps 0

Q 134 RLEPERK 140
 D 106 PLLEPERK 201

RESULT 33
 US-09-198-590-19
 Sequence 18, Application US/09198992
 Patent No. 5834410
 GENERAL INFORMATION:
 APPLICANT: Tjian, Robert
 APPLICANT: Comai, Lucio
 APPLICANT: Dynlacht, Brian D.
 APPLICANT: Hoey, Timothy
 APPLICANT: Ruffell, Geoffrey
 APPLICANT: Tusch, Mark
 APPLICANT: Wang, Edith
 APPLICANT: Weinberg, Robert G.
 TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS
 TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE PATHWAY OF CELL
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEURY, HUBERT, TEST, ALBERTIN & HUBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4197
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/198,592
 FILING DATE: 28-JAN-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Osmen, Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/COCKET NUMBER: A 0960-02/A/T/PAO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 704 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-188-582-18

Query Match 1.63 Score 71.22 41 Length 704
 Best Local Similarity 100.00, Prod No 126402
 Matches 7, Conservation 0, Mismatches 0, Indels 0, Gaps 0

Q 392 STACTSY 398
 D 392 GFADSTV 398

RESULT 34

US-08-646-715-18
 Sequence 19, Application US/08646715
 Patent No. 5837686
 GENERAL INFORMATION:
 APPLICANT: Tjian, Robert
 APPLICANT: Comai, Lucio
 APPLICANT: Dynlacht, Brian D.
 APPLICANT: Hoey, Timothy
 APPLICANT: Ruffell, Geoffrey
 APPLICANT: Tusch, Mark
 APPLICANT: Wang, Edith
 APPLICANT: Weinberg, Robert G.
 TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS
 TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE PATHWAY OF CELL
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEURY, HUBERT, TEST, ALBERTIN & HUBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4197

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,715
 FILING DATE: 28-MAR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Osmen, Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/COCKET NUMBER: A 0960-02/A/T/PAO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 704 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-715-18

Query Match 1.63 Score 71.22 41 Length 704
 Best Local Similarity 100.00, Prod No 126402
 Matches 7, Conservation 0, Mismatches 0, Indels 0, Gaps 0

Q 392 STACTSY 398
 D 392 GFADSTV 398

US-08-640-406-4
 Sequence 4, Application US/08540406
 Patent No. 5837638
 GENERAL INFORMATION:
 APPLICANT: Tjian, Robert
 APPLICANT: Comai, Lucio
 APPLICANT: Dynlacht, Brian D.
 APPLICANT: Hoey, Timothy
 APPLICANT: Ruffell, Geoffrey
 APPLICANT: Tusch, Mark
 APPLICANT: Wang, Edith
 APPLICANT: Weinberg, Robert G.
 TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS
 TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE PATHWAY OF CELL
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEURY, HUBERT, TEST, ALBERTIN & HUBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco


```

GENERAL INFORMATION:
APPLICANT: SCOTT MATTHEW P
              GREGORY HISA V
              HUSBAND, FEMALE
TITLE OF INVENTION: Patched Codes and their use
NUMBER OF SEQUENCES: 10
REFERENCE TO OTHER
PUBLISHED DOCUMENTS:
ADDRESSER: Philip M. Latham, Esq., Attorney at Law
STREET: Four Embarcadero Center, Suite 4100
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS 2.2
SOFTWARE: Patent Release #10, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/067,327-18
FILING DATE: 02-Aug-1997
CLASSIFICATION: unknown.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,093
FILING DATE: unknown
APPLICATION NUMBER: 08/040,406
FILING DATE: unknown
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram J
REGISTRATION NUMBER: 00016
PREFERRED FOR PUBLICATION: YES
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-784,1989
TELEFAX: 415-392,3043
INFORMATION FOR SEQ ID NO.: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: ENI II Nucleo
US-08-918-659-4

Query Match          100% Score 7, TF 4, Length 1111
Best Local Similarity 100%, Start 1, End 1111
Matches      7 / Conserved Domains of Wikipedia    0 / Total 0 Cys 0
               176 SDRGHA 176
                |||||
Do            aaQ QSDGVDA aaQ

RESULT 39
PRT-US95-13233-4
Sequence 4: Application polymorphism
GENERAL INFORMATION:
APPLICANT: THE PART OF INVENTORS OR THE ORGANIZATION OF THE INVENTORS
TITLE OF INVENTION: Patented codes and their use
NUMBER OF SEQUENCES: 10
REFERENCE TO OTHER
PUBLISHED DOCUMENTS:
ADDRESSER: Philip M. Latham, Esq., Attorney at Law
STREET: Four Embarcadero Center, Suite 4100
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS 2.2
SOFTWARE: Patent Release #10, Version #1.00
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: EST0365/1233
FILING DATE: 09-OCT-1990
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Powell, Benjamin I
REGISTRATION NUMBER: 20015
REFERENCE TO FILE NUMBER: 1200-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-7811869
TELEFAX: 415-3881249
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STANDARDNESS: single
ISOLATION: linear
MOLECULE TYPE: protein
PRT US95 1233-4

COPY MATCH: 100%
COPY LOCAL SIMILARITY: 100%
MATCHES: 1, conservative 0, identical 1, nonconservative 0

170 SPECIES: 176
803 SPECIES: 809

RESULT 40
EST0365/496-12
Sequence No. Application: EST0365/496-12
Patent No.: 599281
GENERAL INFORMATION:
APPLICANT: Thompson, Russ Christian
ATTORNEY: Holter, Troy Las
APPLICANT: Elizabeth, Michael
TITLE OF INVENTION: Improved method for the isolation of
NUMBER OF SEQUENCES: 58
CORRESPONDENT ADDRESS:
ADDRESSEE: Fitch & Richardson
STREET: 110 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
DATE: 09-OCT-1994
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: 4.0c to Protein 4.0, version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 540 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 4544 amino acids
TYPE: amino acid
STANDARDNESS:
ISOLATION: linear

Query Match 1.48, Score 6, DE 4, Length 27,
Best Local Similarity 100.0%, Prod No 72,
Matches 4, Conservative 0, Mismatches 0, Indels 0

CY 42 NWSACT 47
ID 8 NWSACT 13

RESULT 44

US-07-668-648-12
Sequence 12, Application US/07-668-648
Patent No. 5416192

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07-668-648
FILING DATE: 1991-08-19
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-668-648-12

Query Match 1.48, Score 6, DE 4, Length 27,
Best Local Similarity 100.0%, Prod No 72,
Matches 4, Conservative 0, Mismatches 0, Indels 0

CY 122 GRLUP 137
ID 5 GRLUP 10

RESULT 45

US-08-428-998-12
Sequence 12, Application US/08-428-998
Patent No. 5883961

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

CY 122 GRLUP 137
ID 5 GRLUP 10

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07-668-648
FILING DATE: 1991-08-19
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07-668-648
FILING DATE: 1991-08-19
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-428-998-12

Query Match 1.48, Score 6, DE 4, Length 27,
Best Local Similarity 100.0%, Prod No 72,
Matches 4, Conservative 0, Mismatches 0, Indels 0

CY 122 GRLUP 137
ID 5 GRLUP 10

RESULT 46

US-08-428-998-12
Sequence 12, Application US/08-428-998
Patent No. 5883961

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-428-998-12

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

TELEPHONE NUMBER: 1-800-444-4444
TELEFAX: 1-800-444-4444
INVENTOR: J. P. Smith, Jr.
TITLE OF INVENTION: IMPROVED METHOD FOR
IDENTIFYING AND MONITORING
TYPE: Utility Model
SUBJECT: 1-800-444-4444
MATERIALS: 1-800-444-4444

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

BY: [Signature]
DATE: 10/10/02

AGENT: [Signature]
DATE: 10/10/02

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

INVENTOR: J. P. Smith, Jr.
Post Office Box 12345
Washington, D.C. 20000-1234

TYPE: unknown
 SPANISH: unknown
 TITLE: unknown
 MODIFIED: 1994-04-10
 MODIFIED BY: 1994-04-10

Query Match: 1.44, Score: 0.00, Length: 0.00
 Best Local Similarity: 1.44, Prod. No.: 0.00
 Matched: 0.00, Mismatched: 0.00, Indels: 0.00

QY 00 PRSAP 04
 1994-04-10
 1994-04-10

RESULT 54
 US 09 471 000A
 1994-04-10
 1994-04-10

APPLICANT: FOWLER, D. M.
 TITLE: INVENTOR
 NUMBER OF SEQUENCES: 10
 ADDRESS: PENNINO & FOWLER
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036 2711

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: DOS/MS DOS
 SOFTWARE: Patent in Release #10, Version #1.05
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 1994/04-10, 0.00
 FILING DATE: 1994-04-10
 CLASSIFICATION: 0.00
 ATTORNEY/AGENT INFORMATION: 0.00
 NAME: MISTOCK, S. Joseph
 REPRESENTATION NUMBER: 1994/04-10
 TELEPHONE: 212 798 1030
 TELEFAX: 212 798 1030
 TELETYPE: 212 798 1030
 MODIFIED: 1994-04-10

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ 1: 0.00
 SEQUENCE INFORMATION: 0.00
 LENGTH: 40 amino acid
 TYPE: amino acid
 STRANDEDNESS: single
 MODIFIED: unknown
 MODIFIED TYPE: 0.00
 MODIFIED BY: 0.00
 MODIFIED DATE: 0.00

Query Match: 1.44, Score: 0.00, Length: 0.00
 Best Local Similarity: 1.44, Prod. No.: 0.00
 Matched: 0.00, Mismatched: 0.00, Indels: 0.00

QY 00 PRSAP 04
 1994-04-10
 1994-04-10

RESULT 54
 US 09 471 000A
 1994-04-10
 1994-04-10

TITLE OF INVENTION: Locally symmetrical Activity Receptor
 NUMBER OF SEQUENCES: 10
 APPLICANT: FOWLER, D. M.
 ADDRESS: PENNINO & FOWLER
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036 2711

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: DOS/MS DOS
 SOFTWARE: Patent in Release #10, Version #1.05
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 1994/04-10, 0.00
 FILING DATE: 1994-04-10
 CLASSIFICATION: 0.00
 ATTORNEY/AGENT INFORMATION: 0.00
 NAME: MISTOCK, S. Joseph
 REPRESENTATION NUMBER: 1994/04-10
 TELEPHONE: 212 798 1030
 TELEFAX: 212 798 1030
 TELETYPE: 212 798 1030

MODIFIED: 1994-04-10
 MODIFIED TYPE: 0.00
 MODIFIED BY: 0.00
 MODIFIED DATE: 0.00

Query Match: 1.44, Score: 0.00, Length: 0.00
 Best Local Similarity: 1.44, Prod. No.: 0.00
 Matched: 0.00, Mismatched: 0.00, Indels: 0.00

QY 00 PRSAP 04
 1994-04-10
 1994-04-10

RESULT 54
 US 09 471 000A
 1994-04-10
 1994-04-10

APPLICANT: FOWLER, D. M.
 TITLE: INVENTOR
 NUMBER OF SEQUENCES: 10
 ADDRESS: PENNINO & FOWLER
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036 2711
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: DOS/MS DOS
 SOFTWARE: Patent in Release #10, Version #1.05
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 1994/04-10, 0.00
 FILING DATE: 1994-04-10
 CLASSIFICATION: 0.00
 ATTORNEY/AGENT INFORMATION: 0.00
 NAME: MISTOCK, S. Joseph
 REPRESENTATION NUMBER: 1994/04-10
 TELEPHONE: 212 798 1030
 TELEFAX: 212 798 1030
 TELETYPE: 212 798 1030
 MODIFIED: 1994-04-10

NAME: MISTOCK, S. Leslie
 REGISTRATION NUMBER: 19,872
 REFERENCE/DOCKET NUMBER: 1101-143
 TELECOMMUNICATION INFORMATION
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 5
 SEQUENCE CHARACTERISTICS
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-471-800-5

Query Match 14%, Score 6, TC 0, Length 38,
 Best Local Similarity 100.0%, Pos: 0, Neg: 0,
 Matches 6, Conservative 0, Mismatches 0, Indels 0

CY 88 FOLSAF 93
 LB 19 FOLSAF 24

RESULT 56
 US-08-471-800-5
 Sequence 5, Application US/09271900
 Patent No. 5852,157
 GENERAL INFORMATION
 APPLICANT: KAY, B. K.
 APPLICANT: FOWLES, D. M.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS
 ADDRESSEE: Pennie & Edwards
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Police #10, Version #1.25
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 08/09471,800
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA
 APPLICATION NUMBER: 08/013,416
 FILING DATE
 ATTORNEY/AGENT INFORMATION
 NAME: Mistock, S. Leslie
 REGISTRATION NUMBER: 19,872
 REFERENCE/DOCKET NUMBER: 1101-143
 TELECOMMUNICATION INFORMATION
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 5
 SEQUENCE CHARACTERISTICS
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-471-800-5

Query Match 14%, Score 6, TC 0, Length 38,
 Best Local Similarity 100.0%, Pos: 0, Neg: 0,
 Matches 6, Conservative 0, Mismatches 0, Indels 0

CY 88 FOLSAF 93
 LB 19 FOLSAF 24

RESULT 57
 US-08-471-068-5
 Sequence 5, Application US/09271900
 Patent No. 5852,157
 GENERAL INFORMATION
 APPLICANT: KAY, B. K.
 APPLICANT: FOWLES, D. M.
 TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 NUMBER OF SEQUENCES: 186
 CORRESPONDENCE ADDRESS
 ADDRESSEE: Pennie & Edwards
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Police #10, Version #1.25
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 08/09471,800
 FILING DATE
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA
 APPLICATION NUMBER: 08/013,416
 FILING DATE
 ATTORNEY/AGENT INFORMATION
 NAME: MISTOCK, S. Leslie
 REGISTRATION NUMBER: 19,872
 REFERENCE/DOCKET NUMBER: 1101-143
 TELECOMMUNICATION INFORMATION
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 5
 SEQUENCE CHARACTERISTICS
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-471-068-5

Query Match 14%, Score 6, TC 0, Length 38,
 Best Local Similarity 100.0%, Pos: 0, Neg: 0,
 Matches 6, Conservative 0, Mismatches 0, Indels 0

CY 88 FOLSAF 93
 LB 19 FOLSAF 24

RESULT 58
 US-08-706-3440-7
 Sequence 5, Application US/09271900
 Patent No. 6249555
 GENERAL INFORMATION
 APPLICANT: TAMEI, KUNOLPH
 APPLICANT: MASCO, WILMA
 TITLE OF INVENTION: Genetic Alterations Related to Familial
 TITLE OF INVENTION: Alzheimer's Disease
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS
 ADDRESSEE: Pennie & Edwards
 STREET: 1155 Avenue of the Americas, Suite 600

CITY: WASH DCTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20004-4444
 MODER: REAR ARCH P RM
 MODER TYPE: floppy disk
 COMPUTER: IBM pc comp at lab
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Pat on In Release #113, Version #1.00
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 09/706/00444
 FILING DATE: 30 Apr 1996
 CLASSIFICATION: 300
 PUBLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: KIM, JUDITH D
 REGISTRATION NUMBER: 47,671
 REFERENCE/ORDER NUMBER: 0949, 414000
 TELEPHONE: 202-331-1632
 TELEFAX: 202-331-1636
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not known
 MULTIPLE TYPE: peptide
 DS: 09-905-744b-6

Query March 1, 483 Score 62.00 42.10000000
 Best Local Similarity: 100.0% Prod. No. 002
 Matches: 62 Conserved: 00 Mismatches: 02 Gaps: 02

RESULT 01
 DS: 09-905-744b-6
 Sequence 33, Application: 090904444A
 Patent No. 6197852
 GENERAL INFORMATION:
 APPLICANT: KAYOS, Steven L
 TITLE OF INVENTION: METHOD FOR DETERMINING THE P
 NUMBER OF SEQUENCES: 47
 ADDRESS/AGENT ADDRESS:
 ADDRESS: Pharmacal & Biotech Co., 10000 10th St NW
 STREET: 101 Hennepin Ave
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 49001
 MODER REAR ARCH P RM
 MODER TYPE: floppy disk
 COMPUTER: IBM pc comp at lab
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Pat on In Release #113, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/706/00444
 FILING DATE:
 CLASSIFICATION: 48
 ATTORNEY/AGENT INFORMATION:
 NAME: DARTLEY, J. J. James D
 REGISTRATION NUMBER: 84,000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 616/843-2010
 TELEFAX: 616/843-8807
 TELEX: 224401
 INFORMATION FOR SEQ ID NO: 33
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MULTIPLE TYPE: peptide
 DS: 09-905-744b-6

Query March 1, 483 Score 62.00 42.10000000
 Best Local Similarity: 100.0% Prod. No. 002
 Matches: 62 Conserved: 00 Mismatches: 02 Gaps: 02

DS: 09-905-744b-6
 Sequence 33, Application: 090904444A
 Patent No. 6197852
 GENERAL INFORMATION:
 APPLICANT: KAYOS, Steven L
 TITLE OF INVENTION: METHOD FOR DETERMINING THE P
 NUMBER OF SEQUENCES: 47
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 ADDRESS: Pharmacal & Biotech Co., 10000 10th St NW
 STREET: 101 Hennepin Ave
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 49001
 MODER REAR ARCH P RM
 MODER TYPE: floppy disk
 COMPUTER: IBM pc comp at lab
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Pat on In Release #113, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/706/00444
 FILING DATE:
 CLASSIFICATION: 48
 ATTORNEY/AGENT INFORMATION:
 NAME: DARTLEY, J. J. James D
 REGISTRATION NUMBER: 84,000
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 TELEX: 224401
 INFORMATION FOR SEQ ID NO: 33
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MULTIPLE TYPE: peptide
 DS: 09-905-744b-6

TELEPHONE: 66191 608-5007
 TELEFAX: 66191 608-5000
 TELEX:
 INFORMATION FOR SEQ ID NO: 113
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 DS: 09-905-744b-6

Query March 1, 483 Score 62.00 42.10000000
 Best Local Similarity: 100.0% Prod. No. 002
 Matches: 62 Conserved: 00 Mismatches: 02 Gaps: 02

DS: 09-905-744b-6
 Sequence 33, Application: 090904444A
 Patent No. 6197852
 GENERAL INFORMATION:
 APPLICANT: KAYOS, Steven L
 TITLE OF INVENTION: METHOD FOR DETERMINING THE P
 NUMBER OF SEQUENCES: 47
 ADDRESS/AGENT ADDRESS:
 ADDRESS: Pharmacal & Biotech Co., 10000 10th St NW
 STREET: 101 Hennepin Ave
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 49001
 MODER REAR ARCH P RM
 MODER TYPE: floppy disk
 COMPUTER: IBM pc comp at lab
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Pat on In Release #113, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/706/00444
 FILING DATE:
 CLASSIFICATION: 48
 ATTORNEY/AGENT INFORMATION:
 NAME: DARTLEY, J. J. James D
 REGISTRATION NUMBER: 84,000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 616/843-2010
 TELEFAX: 616/843-8807
 TELEX: 224401
 INFORMATION FOR SEQ ID NO: 33
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MULTIPLE TYPE: peptide
 DS: 09-905-744b-6

Query March 1, 483 Score 62.00 42.10000000
 Best Local Similarity: 100.0% Prod. No. 002
 Matches: 62 Conserved: 00 Mismatches: 02 Gaps: 02

DS: 09-905-744b-6
 Sequence 33, Application: 090904444A
 Patent No. 6197852
 GENERAL INFORMATION:
 APPLICANT: KAYOS, Steven L
 TITLE OF INVENTION: METHOD FOR DETERMINING THE P
 NUMBER OF SEQUENCES: 47
 ADDRESS/AGENT ADDRESS:
 ADDRESS: Pharmacal & Biotech Co., 10000 10th St NW
 STREET: 101 Hennepin Ave
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 49001
 MODER REAR ARCH P RM
 MODER TYPE: floppy disk
 COMPUTER: IBM pc comp at lab
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Pat on In Release #113, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/706/00444
 FILING DATE:
 CLASSIFICATION: 48
 ATTORNEY/AGENT INFORMATION:
 NAME: DARTLEY, J. J. James D
 REGISTRATION NUMBER: 84,000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 616/843-2010
 TELEFAX: 616/843-8807
 TELEX: 224401
 INFORMATION FOR SEQ ID NO: 33
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MULTIPLE TYPE: peptide
 DS: 09-905-744b-6


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US-09-511-485-16
Sequence 16, Application US/090511485
Patent No. 5912912
GENERAL INFORMATION
APPLICANT: KOTTELNIK, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY PRIMERS.
TITLE OF INVENTION: PRIMERS AND DETECTION METHODS.
NUMBER OF SEQUENCES: 38
REFERENCE/AGENT ADDRESS
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-09-1995
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07947/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-5096
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
SPARSINESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-09-511-485-16

Query Match 1 4% Score 67 of 21 Length 68
Best Local Similarity 100.0% Fred No. 1 To 20
Matches 69 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 43 VSASTL 48
|||||
DQ 17 VSASTL 22

RESULT 62
US-09-511-485-17
Sequence 17, Application US/090511485
Patent No. 5912912
GENERAL INFORMATION
APPLICANT: KOTTELNIK, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY PRIMERS.
TITLE OF INVENTION: PRIMERS AND DETECTION METHODS.
NUMBER OF SEQUENCES: 39
REFERENCE/AGENT ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-09-1995
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07947/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-5096
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
SPARSINESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-09-511-485-17

Query Match 1 4% Score 67 of 21 Length 68
Best Local Similarity 100.0% Fred No. 1 To 20
Matches 69 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 43 VSASTL 48
|||||
DQ 17 VSASTL 22

RESULT 63
US-09-091-725-27
Sequence 27, Application US/09091725
Patent No. 629141
GENERAL INFORMATION
APPLICANT:
TITLE OF INVENTION: Tissue-specific DNA probes for use in diagnosis
TITLE OF INVENTION: and recombinant DNA for use in diagnosis
NUMBER OF SEQUENCES: 51
REFERENCE/AGENT ADDRESS:
ADDRESS: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20006-1089
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.35 (VPMO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-09-1995
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
REFERENCE/AGENT ADDRESS:
ADDRESS: E. Victor Donahue
STREET: 35-402
CITY:
STATE:
COUNTRY:
ZIP:
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-725-27

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ENTRY NAME: [REDACTED] DATE: [REDACTED] TIME: [REDACTED]
 FILE NAME: [REDACTED] FILE TYPE: [REDACTED]
 MAP NAME: [REDACTED] MAP TYPE: [REDACTED]

27. [REDACTED]

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2. [REDACTED]

3. [REDACTED]

4. [REDACTED]

5. [REDACTED]

6. [REDACTED]

7. [REDACTED]

8. [REDACTED]

9. [REDACTED]

10. [REDACTED]

11. [REDACTED]

12. [REDACTED]

13. [REDACTED]

14. [REDACTED]

15. [REDACTED]

16. [REDACTED]

17. [REDACTED]

18. [REDACTED]

19. [REDACTED]

20. [REDACTED]

21. [REDACTED]

22. [REDACTED]

23. [REDACTED]

24. [REDACTED]

25. [REDACTED]

26. [REDACTED]

27. [REDACTED]

28. [REDACTED]

29. [REDACTED]

30. [REDACTED]

31. [REDACTED]

32. [REDACTED]

33. [REDACTED]

34. [REDACTED]

35. [REDACTED]

36. [REDACTED]

37. [REDACTED]

38. [REDACTED]

39. [REDACTED]

40. [REDACTED]

41. [REDACTED]

28. [REDACTED]

1. [REDACTED]

2. [REDACTED]

3. [REDACTED]

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7. [REDACTED]

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9. [REDACTED]

10. [REDACTED]

11. [REDACTED]

12. [REDACTED]

13. [REDACTED]

14. [REDACTED]

15. [REDACTED]

16. [REDACTED]

17. [REDACTED]

18. [REDACTED]

19. [REDACTED]

20. [REDACTED]

21. [REDACTED]

22. [REDACTED]

23. [REDACTED]

24. [REDACTED]

25. [REDACTED]

26. [REDACTED]

27. [REDACTED]

28. [REDACTED]

29. [REDACTED]

30. [REDACTED]

31. [REDACTED]

32. [REDACTED]

33. [REDACTED]

34. [REDACTED]

35. [REDACTED]

36. [REDACTED]

37. [REDACTED]

38. [REDACTED]

39. [REDACTED]

40. [REDACTED]

41. [REDACTED]

[illegible]

Country	Year	Population (millions)	Population density (per sq. km)	Urban population (millions)	Urban population density (per sq. km)	Urban population as % of total
Algeria	1970	10.0	100	3.0	100	30
Algeria	1980	12.0	120	4.0	120	33
Algeria	1990	14.0	140	5.0	140	36
Algeria	2000	16.0	160	6.0	160	38
Algeria	2010	18.0	180	7.0	180	39
Algeria	2020	20.0	200	8.0	200	40
Algeria	2030	22.0	220	9.0	220	41
Algeria	2040	24.0	240	10.0	240	42
Algeria	2050	26.0	260	11.0	260	42
Algeria	2060	28.0	280	12.0	280	43
Algeria	2070	30.0	300	13.0	300	43
Algeria	2080	32.0	320	14.0	320	44
Algeria	2090	34.0	340	15.0	340	44
Algeria	2100	36.0	360	16.0	360	44
Algeria	2110	38.0	380	17.0	380	45
Algeria	2120	40.0	400	18.0	400	45
Algeria	2130	42.0	420	19.0	420	45
Algeria	2140	44.0	440	20.0	440	45
Algeria	2150	46.0	460	21.0	460	46
Algeria	2160	48.0	480	22.0	480	46
Algeria	2170	50.0	500	23.0	500	46
Algeria	2180	52.0	520	24.0	520	46
Algeria	2190	54.0	540	25.0	540	46
Algeria	2200	56.0	560	26.0	560	46
Algeria	2210	58.0	580	27.0	580	47
Algeria	2220	60.0	600	28.0	600	47
Algeria	2230	62.0	620	29.0	620	47
Algeria	2240	64.0	640	30.0	640	47
Algeria	2250	66.0	660	31.0	660	47
Algeria	2260	68.0	680	32.0	680	47
Algeria	2270	70.0	700	33.0	700	47
Algeria	2280	72.0	720	34.0	720	47
Algeria	2290	74.0	740	35.0	740	47
Algeria	2300	76.0	760	36.0	760	47
Algeria	2310	78.0	780	37.0	780	47
Algeria	2320	80.0	800	38.0	800	48
Algeria	2330	82.0	820	39.0	820	48
Algeria	2340	84.0	840	40.0	840	48
Algeria	2350	86.0	860	41.0	860	48
Algeria	2360	88.0	880	42.0	880	48
Algeria	2370	90.0	900	43.0	900	48
Algeria	2380	92.0	920	44.0	920	48
Algeria	2390	94.0	940	45.0	940	48
Algeria	2400	96.0	960	46.0	960	48
Algeria	2410	98.0	980	47.0	980	48
Algeria	2420	100.0	1000	48.0	1000	48
Algeria	2430	102.0	1020	49.0	1020	48
Algeria	2440	104.0	1040	50.0	1040	48
Algeria	2450	106.0	1060	51.0	1060	48
Algeria	2460	108.0	1080	52.0	1080	48
Algeria	2470	110.0	1100	53.0	1100	48
Algeria	2480	112.0	1120	54.0	1120	48
Algeria	2490	114.0	1140	55.0	1140	48
Algeria	2500	116.0	1160	56.0	1160	48
Algeria	2510	118.0	1180	57.0	1180	48
Algeria	25					

Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses (Y-axis) is plotted against the number of trials (X-axis). The data shows a positive correlation between the number of trials and the number of correct responses, with a slight increase in the number of correct responses as the number of trials increases.

1 FRONT 18
2 IN 39 40 39A /
3 Surname / Applicant (in full), Mr
4 Phone: 0550000
5 GENERAL INFORMATION
6
7 APPLICANT: KAYLIE, 30/01/86
8 APPLICANT: MOTHER, MARGARET
9 TITLE OF INVENTION: VERBOWE STEPS
10 NUMBER OF SHEETS: 14
11 PREFERRED ADDRESS
12
13 APPLICANT: Mrs M. Kaylie
14 ADDRESS: 44, Boxgrove Drive, 11

1. *Chlorophyll a* and *Chlorophyll b* were determined using a spectrophotometer (Shimadzu UV-1601) at 663 nm and 646 nm, respectively. The concentration of chlorophyll was calculated using the following formula: $\text{Chlorophyll } a = 11.85 \times \text{OD}_{663} - 1.81 \times \text{OD}_{646}$ and $\text{Chlorophyll } b = 22.9 \times \text{OD}_{646} - 4.68 \times \text{OD}_{663}$ (Arar and Parsons, 1972).

